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Total number of hits satisfying chosen parameters:
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Perfect score:
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    Score
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Listing first 45 summaries
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US-08-474-068A-6
US-08-188-228-48
US-08-188-228-48
US-08-332-643-42
US-08-332-643-56
US-08-332-643-56
US-08-332-643-56
US-08-332-643-56
US-08-332-643-59
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US-08-474-068A-7
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; Patent No. <u>5620855</u>
; GENERAL INFORMATION:
; APPLICANT: Anne H.
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US-08-431-560-1
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%
Matches 832; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 04-FEB-1S
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Anne H. Dantzig, et al.
TITLE OF INVENTION: Mammalian Influx Peptide
TITLE OF INVENTION: Transporter
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Macintosh
OPERATING SYSTEM: Macinto
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
121 DNRPTFLQSKYEGSVRQNSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLPMINNVMYF
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/431, FILING DATE: 01-MAY-1995 CLASSIFICATION: 435
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US-08-474-066A-8
US-08-474-066A-8
US-08-472-481-7
US-08-237-919-2
US-08-732-429-2
US-09-798-267-2
US-09-798-267-3
PCT-US95-05518-2
US-09-187-859-25
US-09-187-859-25
US-08-738-349-4
US-08-738-349-6
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Pred. No. 0;
0; Mismatches
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Minimum Maximum

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Sequence Sequence Sequence

Appli Appli

Sequence Sequence Sequence Sequence

Sequence

Sequence:

Database

DB 0

Length Indels

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RESULT 2
US-08-463-345-1
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Patent NO. 571
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NUMBER OF S
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ADDRESSEE
STREET:
CITY: In
STATE: I
COUNTRY:
ZIP: 462
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                                        ADDRESSEE: Bil Lilly and CC
STREET: Lilly Corporate Cer
CITY: Indianapolis
STATE: IN
COUNTRY: U.S.A.
ZIP: 46285
COMPUTER REALDABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: MICROSOft WORD
SOFTWARE: MICROSOft WORD
COMPUTER: MACINTOSH
OPERATING SYSTEM: MORD
CONTRAIN DATA:
OPERATING SYSTEM: MORD
SOFTWARE: MICROSOFT
SOFTWARE: MICROSOFT
APPLICATION DATA:
                                                                                                                                                                                APPLICANT: Anne H. Dai
TITLE OF INVENTION: M:
TITLE OF INVENTION: T
NUMBER OF SEQUENCES:
                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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            APPLICATION NUMBER: FILING DATE: 05-JUN CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                      GIPTVGMAVGILLTTLLVIGIILAVVFIRIKKDKGKDNVESAQASEVKPLRS 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIEVSDKDFKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTNIGSTILTIQATDADEP
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APPLICATION DATA:
                                                                                                                                                                                                        Anne H. Dantzig, et al
/ENTION: Mammalian Inf
                      NUMBER: US/08/463,
05-JUN-1995 ►
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; APPLICATION NUMBER: US 08,
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 832 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-463-345-1
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Best Local Similarity
Matches 832; Conserv
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GIPTVGMAVGILLTTLLVIGIILAVVFIRIKKDKGKDNVESAQASEVKPLRS
                                                                                                                                         SLRGDTRGWLKIDHVTGEIFSVAPLDREAGSPYRVQVVATEVGGSSLSSVSEFHLILMDV
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                                                                                            NDNPPRLAKDYTGLFFCHPLSAPGSLIFEATDDDQHLFRGPHFTFSLGSGSLQNDWEVSK
                                                                                                                                                                                      FGVKYNASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVAIGTKVGNVTAKDPEGLDISY
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                                              INGTHARLSTRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVTFCSCVEGSCFRPAGHQT
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; Pred. No. 0;
0; Mismatches
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Best Local Similarity
Matches 209; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31.815
REFERENCE/DOCKET NUMBER: P-LJ 1682
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 14-MAY-1994 PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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366 GLSNTATAVITVTDVNDNPPEFTAMTFYGEV---PENRVDVIVANLTVTDKDQPHTPAWN 422
                                                                                                                                                 246 DVNGNQVENPIDIVINVIDMNDNRPEFLHQVWNGTVPEGSKPGTYVMTVTAIDADDPNAQ 305
                                                                                                                                                                         314 DEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEVQENERLGNSIGTLTAHDRDEENTA 373
                                                                                                                                                                                                                                                                 270 QYSLVDKEKLPRFPFSI-----DQ-------EGDIYVTQPLDREEKDAYVFYAVAK 313
                                                                                                                                                                                                                                                                                                       137 EKDQKKIEDIIFPWQQYKDSSHLKRQKRDWVIP-PINLPENSRGPFPQELVRIR-----
                                                                                                                                                                                                                                                                                                                                               229 SYDIIVTENI -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 FLOSKYEGSVRONSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLPMINNVMYFQIN-- 183
                                                                                                                                                                                                                                                                                                                                                                                 82 EDFRVGEDGVVYAERSFQLSAEPTE----FVVSARDKETQEEWQMKVKLTPEPAFTGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 FPEDVHSAVVSRSVHGGQPLLNVRFQSCDE
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                                                                         NGMLRYRILSQAPSSPSPNMFTINNETGDIITVAAGLDREKVQQYTLIIQATDMEGNPTY
                                                                                                             NSFLNYRIVEQTPKLPMDGLFLIQTYAGMLQLAKQSLKKQDTPQYNLTIEVSDKD-----
                                                                                                                                                                                                                             ----SDRDKSLSLRYSVTGPGADQPPTGIFIINPISGQLSVTKPLDREQIASFHLRAHAV
                                   -FKTLCFVQINVIDINDQIPIF-EKSDYGNLTLAEDTNIGSTILTIQATDADEPFTGSSK 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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30-OCT-1990
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Pred. No. 6.9e-53;
7; Mismatches 328;
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RESULT 4
US-08-474-068A-6
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Query Match 16.1%; Score 696; DB 2; 1
Best Local Similarity 26.9%; Pred. No. 6.9e-53;
Matches 209; Conservative 117; Mismatches 328;
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                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/607,293 FILING DATE: 30-OCT-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 14-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acid
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CITY: San Diego
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                                                                                                                                                                                                                                                                     NAME: Campbell, Cathryn A REGISTRATION NUMBER: 31,8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGHQTGIPTV---GMAVGILLTTLLVIGIILAVVFIRIKKDKGKDNVESAQASEVKP 829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVAIGTKVGNVTAKDP----EGLDISYSL 602
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                                                                                                                 amino acid
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SYSTEM: PC-DOS/MS-DOS
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                                  Length 913;
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Indels 124;

Gaps

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RESULT 5
US-08-472-481-5
; Sequence 5, Application US/08472481
; Patent No. 5863804
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                                                                                                                                                                                                                                GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                               APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadherin Adhesion
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                  716
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                                                                                                                   CITY: San Diego
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                                                                                  COUNTRY:
                                                                                                                                     STREET:
                                                                                                                                                   ADDRESSEE:
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4370 La Jolla Village Drive,
                                                                                 United States
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REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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APPLICATION NUMBER: US 08/213,361
FILING DATE: 14-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/607,293
FILING DATE: 30-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 30-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
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                  DVNDNPPRL-AKDYTGLFFCHPLSAPGSLIFEATDDDQHLFRGPHFTFSLGSG--SLQND
                                                                                                                                                                                                                                                                                                                                                                                                DINDNAPQVNPKEAT - - -TCETLQ - PNAINITAVDPDIDPNAGP - FAFELPDSPPSIKRN
                                                                                     RGDTRGWLKIDHVTGEIFSVAPLDREA----GSPYRVQVVATEVGGSSLSSVSEFHLILM
                                                                                                                                                               ASSFAKETLIVTDVNEAPQFSQHVFQAKVSEDVAIGTKVGNVTAKDP----EGLDISYSL
                                                                                                                                                                                                 ARYQMTGGDPTGQFTILTDPNSNDGLVTVVKPIDFETNRMFVLTVAAENQVPLAKGIQHP
                                                                                                                                                                                                                      ILYHIIKGDSEGRLGVDTDPHTNTGYVIIKKPLDFETAAVSNIVFKAENPEPLVFGVKYN
                                                                                                                                                                                                                                                                  GLSNTATAVITVTDVNDNPPEFTAMTFYGEV---PENRVDVIVANLTVTDKDQPHTPAWN
                                                                                                                                                                                                                                                                                                                                                               NSFLNYRIVEOTPKLPMDGLFLIQTYAGMLQLAKQSLKKQDTPQYNLTIEVSDKD-----
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                                                                                                                                PQSTATVSITVIDVNESPYFVPNPKLVRQEEGLLAGSMLTTFTARDPDRYMQQTSLRYSK
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                                                                 LSDPANWLKIDPVNGQITTTAVLDRESIYVQNNMYNATFLASDNGIPPMSGTGTLQIYLL
                                                                                                                                                                                                                                                                                                 -FKTLCFVQINVIDINDQIPIF-EKSDYGNLTLAEDTNIGSTILTIQATDADEPFTGSSK
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07-JUN-1995
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                                                                                                                                                                                                                                                       Query Match 15.8
Best Local Similarity 29.3
Matches 176; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5597725and, Greta E
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 3134
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                   290 SKPGTYVMTITANDADDSTTANGMYRYRIVTQTPQSPSQNMFTINSETGDIVTVAAGWDR 349
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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QDTPQYNLTIEVSDKD-----FKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTNIG 466
                                                                     ERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTPKLPMDGLFLIQTYAGMLQLAKQSLKK 412
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                                                                                                           YVTRPMDREEHASYHLRAHAVDMNGNKVENPIDLYIYVIDMNDNHPEFINQVYNCSVDEG
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                                                                                                                                                                                                                                                       Score 684.5; DB 1;
Pred. No. 7.3e-52;
6; Mismatches 288;
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RESULT 7
US-08-332-643-42
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Sequence 563963
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                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: NO. 5639634and, Greta
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: CADHERIA
                     SEQUENCE CHARACTERISTICS:
                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                               TELEFAX:
                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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LENGTH:
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WESULT 8
US-08-332-638-48
US-08-332-638-48
; Sequence 48, Application US/08332638
; Patent No. 5646550
; GENERAL INFORMATION:
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Best Local
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                              APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS
NUMBER OF SEQUENCES: 62
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                                                               ADDRESSEE: Marshi
ADDRESSEE: Borun
STREET: 6300 Sea
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QDTPQYNLTIEVSDKD-----FKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTNIG
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                                                                                                                                6300 Sears Tower,
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Pred. No. 7.3
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                                                                                                                                S. Wacker Drive
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; MOLECULE TYPE: protein
US-08-332-638-48
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48
SEQUENCE CHARACTERISTICS:
LENGTH: 916 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.8%; Score 684.5; Best Local Similarity 29.3%; Pred. No. 7.3e Matches 176; Conservative 106; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: NO. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
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   817
                                    705 IIKVKVCPCDDNGDCTTIG---AVAAAGLGTGAIVAILICILILLTMVLLEVMWMKRREK
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                                                                                                   GPYVFELPFVPAAVRKNWTITRLNGDYAQLSLRILYLEAGMYDVPIIVTDSGNPPLSNTS
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                                                                   SLPVTFCSCVEGSCFRPAGHQTGIPTVGMAVGILLTTLLVIGIILAVV--FIRIKKDKGK
                                                                                                                                    GPH-FTFSLGSGSLQNDWEVSKINGTHARLSTRHTDFEERAYVVLIRINDGGRPPLEGIV
                                                                                                                                                                   ADNGIPPASGTGTLQIYLIDINDNAPELLPKEAQICERPNLNA---INITAADADVHPNI
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-188-228-62
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US-08-188-228-62
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APPLICATION NUMBER: US 08/049,460

FILING DATE: 19 APR 1993

PRIOR APPLICATION DATA:

APPLICATION UMBER: US 07/872,643

FILING DATE: 17 APR 1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 5597725and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEPHONE: (312) 474-6300

TELEPHONE: (312) 474-6300

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Patent No. 5597725
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 15.2%; Score 657.5; DB 1; Best Local Similarity 28.7%; Pred. No. 1.2e-49; Matches 199; Conservative 104; Mismatches 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
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TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  212 SVKDMGGQSEN--SFSDTTSV-----DIIVTENIWKAPKPVEMVENSTDPHPIKITQVRW 264
                                                                                                                                                                                                                                                                                                                                                                                                                            160 NGQLYYQIVIQLPMINNVMYFQINNKTGAISL---TREGSQELNPAKNPSYN-----LVI 211
    274
                             369 EENTANSFLNYRIVEQTPKLPMDGLFLIQTYAG-MLQLAKQSLKKQDT---PQYNLTIEV 424
                                                                                                                        309 YAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEVQENERLGNSIGTLTAHDRD 368
                                                                                                                                                                                         163 -----VDSDRPERSKFRLTGKGVDQEPKGIFRINENTGSVSVTRTLDREVIAVYQL 213
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                                                                                                                                                                                                                                                                                    113 GGKDIOGSLODIFKFARTSPVPRQKRSIVVS------PILIPENQRQPFPRDVGKV-- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                             61 NDKLRYEV-----SSPYFKVNSDGGLVALRNITAVGKTLFVHARTPHAEDMAELVIV 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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DPATDNALLRYNIRQQTPDKPSPNMFYIDPEKGDIVTVVSPALLDRETLENPKYELIIEA 333
                                                                                           FVETTDVNGKTLEGPVPLEVIVIDQNDNRPIFREGPYIGHVMEGSPTGTTVMRMTAFDAD
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TED. PLOCETI	•
linear	lin
mino acid	; TYPE: amino acid
	; SEQUENCE CHARACTERIS
25-3856 FOR SEQ ID NO: 56:	; INFORMATION FOR SEQ ID
X: (312) 984-9740	X: (312)
NOITA	NOITA
ITION NUMBER: 35,302 E/DOCKET NUMBER: 27866/30795	; REGISTRATION NUMBER: 3 ; REFERENCE/DOCKET NUMBER
Gre	NAME: No. 56
: THEODY ATTOM:	DATE:
ICATION DATA: ION NUMBER: US/07/872,643	; PRIOR APPLICATION DATA:
CATION: 435	CLASSIFICATION: 4
TION NUMBER: US/08/332,643	APPLICATION NUMBER:
PatentIn Release # LICATION DATA:	; SOFTWARE: PatentI; CURRENT APPLICATION
SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM:
TYPE: Floppy disk	; MEDIUM TYPE: Flop
READABLE FORM:	COMPUTER READABLE FO
USA	COUNTRY: USA
Illinois	; CITY: Chicago ; STATE: Illinois
Two First National Plaza, 20 South Clark	Two
E: Marshall, O'Toole, Gerstein, Murray &	SSEE:
ADDRE:	: CORRESPONDENCE ADDRE
NVENTION:	F INVENTION:
	AL INF
Application 05/00332043	tent No. 5
1	643-
SCRNSKVDCNAAGALRESLPSVILLS 706	db 679 VCSCRNSKVDCNAAG
MAVG	Qy 764 FCSCVEGSCFRPA
NTHALVSLLQ-NLNKANYNLPIMVTDSGKP	Db 620 FEIHKQAVPDKVWKI
LGSGSLQND-WEVSKINGTHARLSTRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVT 76:	Oy 705 FSLGSGSLQND-WEV
JEDVNDNAPFIYPTVAEVCDDAKNLSVVILGASDKDLHPNTDP-FK 619	Ap-
PPRLAKDYTGLF	Qy 653 FHLILMDVNDNPPRL
TIRYSVYKDPAGWLNINPINGTVDTTAVLDRESPFVDNSVYTALFLAIDSGNPPATGTGT 570	Db 511 TIRYSVYKDPAGWLN
KIDHVTGEIFSVAPLDREAGSPYRVQV	Qy 598 -ISYSLRGDTRGWLK
VPDVSYGPSSTATVHITVLDVNEGPVFYPDPMMVTRQEDLSVGSVLLTVNATDPDSLQHQ 510	Db 451 VPDVSYGPSSTATVH
FGVKYNASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVAIGTKVGNVTAKDPEGLD 597	Qy 540 VFGVKYNASSFAKET
PTTGAWRAAYTIINGNPGQSFEIHTNPQTNEGMLSVVKPLDYEISAFHTLLIKVENEDPL 450	Db 391 PTTGAWRAAYTIING
SSKILYHIIKGDSEGRLGVDTDPHTNTGYVIIKKPLDFETAAVSNIVFKAENPEPL 539	Qy 480 PFTGSSKILYHIIKG
FQATVE	Db 334 QDMAGLDVGLTGTAT
DFKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTNIGSTILTIQATDAD	1

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US-08-332-638-62
; Sequence 62, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                           APPLICANT: Suzuki, Shintaro
                                                       STATE: Illi
COUNTRY: US
ZIP: 60606
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                                                                                                              STREET:
CITY: C
                                                                                                                             ADDRESSEE: Marshall, O'Toole, ADDRESSEE: Borun STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                          VCSCRNSKVDCNAAGALRFSLPSV----ILLS
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                                                                                                                                                                 Gerstein,
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Best Local Similarity
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APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 62:
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LENGTH: 713 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: NO. 5646250and, Greta
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NDKLRYEV-----SSPYFKVNSDGGLVALRNITAVGKTLFVHARTPHAEDMAELVIV 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: PatentI
                                                     LLITLEDVNDNAP-----FIYPTVAEVCDDAKNLSVVILGASDKDLHPNTDP-FK
                                                                                                                                                                                                                                                                                                    PFTGSSKILYHIIKGDSEGRLGVDTDPHTNTGYVIIKKPLDFETAAVSNIVFKAENPEPL
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                 FSLGSGSLQND-WEVSKINGTHARLSTRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVT
                                                                                         FHLILMDVNDNPPRLAKDYTGLFFCHPLSAP----
                                                                                                                           TIRYSVYKDPAGWLNINPINGTVDTTAVLDRESPFVDNSVYTALFLAIDSGNPPATGTGT
                                                                                                                                              VFGVKYNASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVAIGTKVGNVTAKDPEGLD--
                                                                                                                                                                                                                                                                          PTTGAWRAAYTIINGNPGQSFEIHTNPQTNEGMLSVVKPLDYEISAFHTLLIKVENEDPL
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                                                                                                                                                                                                   VPDVSYGPSSTATVHITVLDVNEGPVFYPDPMMVTRQEDLSVGSVLLTVNATDPDSLQHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (312) 474-6300
15.2%;
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Pred. No. 1.2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31340
---GSLIFEATDDDQHLFRGPHFT
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Indels 105; Length

Gaps

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597 450 539 390 479 333 424 368

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US-08-453-702A-98
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 555 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: No. 5891706and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Protocadherin Materials and Methods NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                          406 AKQSLKKQDTPQYNLTIEVSDKD-----FKTLCFVQINVIDINDQIPIF-EKSDYGNLT 458
                                                                                                                                                                                                                                             346 VFEVQENERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTPKLPMDGLFLIQTYAGMLQL 405
                                                                                                                                                                                                                                                                                                                                            287 DQ-EGDIYVTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVT 345
                                                                                                                                                                                                                                                                                                                                                                                                                        239 WKAPKPVEMVENSTDPHPIKITQVRWN-------DPGAQYSLVDKEKLPRFPFSI 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  764 FCSCVEG--SCFRPAGHOTGIPTVGMAVGILLT 794
  519 LDFETAAVSNIVFKAENPEPLVFGVKYNASSFAKFTLIVTDVNEAPQFSQHVFQAKVSED 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 233 SOCITY: Chicago STATE: Illino:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                      54 NPISGQLSVTKPLDRELIARFHLRAHAVDINGNQVENPIDIVINVIDMNDNRPEFLHQVW 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray,
                                                                                                                                                                                                                                                                                                                                                                                           2 WVIP-PINLPENSRGPFPQELVRIRSDRDKNLSLRYSVTGPGA------DQPPTGIFII 53
                                               --PENRVDVIVANLTVTDKDQPHTPAWNAAYRISGGDPTGRFAILTDPNSNDGLVTVVKP
                                                                                     LAEDTNIGSTILTIQATDADEPFTGSSKILYHIIKGDSEGRLGVDTDPHTNTGYVIIKKP 518
                                                                                                                               VAAGLDREKVQQYTLIIQATDMEGNPTYGLSNTATAVITVTDVNDNPPEFTAMTFYGEV-
                                                                                                                                                                                                                     NGSVPEGSKPGTYVMTVTAIDADDPNALNGMLRYRILSQAPSTPSPNMFTINNETGDIIT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEIHKQAVPDKVWKISKINNTHALVSLLQ-NLNKANYNLPIMVTDSGKPPMTNITDLRVQ 678
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US-08-474-067-7
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                                                                                                                                                                                                                                                                                                                            TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/607,293 FILING DATE: 30-OCT-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,361
FILING DATE: 14-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NUMBER OF SEQUENCES:
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                                               112 WVIP-PISCLENHRGPYPMRLVQIKSNKDKESKVYYSITGQGADSPPVGIFIIERETGWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 IDFETNRMFYLTVAAENQVPLAKGIQHPPQSTATVSVTVIDVNENPYFAPNPKIIRQEEG
    293 YVTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEVQEN 352
                                                                                   239 WKAPKPVEMVENSTDPHPIKITQVRWN---DPGAQYSLVDK--EKLPRFPFSIDQE-GDI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        521 IIITDSGNPPKSNISILRVKVCQCDSNGDC 550
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                                                                                                                                                                                                                                                             LENGTH:
TYPE: a
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                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
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CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                  189;
                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                               837 amino acids
                                                                                                                               Conservative
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                                                                                                                                                                                                                                         linear
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                       (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                    14.7%; Score 634; DB 2 30.4%; Pred. No. 2e-47;
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RESULT 14
US-08-474-068A-7
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GENERAL INFORMATION:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 14-MAY-1994
PRIOR APPLICATION DATA:
                                     APPLICATION NUMBER: US 07/607,293 FILING DATE: 30-OCT-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CITY: S
STATE:
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                                                                                                                                                                         APPLICATION NUMBER: US/OFFILING DATE: 07-JUN-1995
CLASSIFICATION: 514
   NAME: Campbe
REGISTRATION
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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: California
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                     Campbell,
                                                                                                                                                                                                                                                                                                                                                                                                                           4370 La Jolla
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                                                                                                                                                                                                                                                                                                                                                                       United States
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70 La Jolla Village Dr
     NUMBER:
 Cathryn A.
BER: 31,815
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US-08-472-481-6
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                                                                                                                                                                       Sequence 6, Application Patent No. 5863804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local :
                                                                                           GENERAL INFORMATION:
APPLICANT: Ranscht,
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 837 amino acids
TYPE: amino acid
                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171
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                                                                                                                                                                                                                                                                                           685
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                                   ADDRESSEE:
STREET: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKPGTSVMTVNATDADDAVNTDNGIVSYSIVSQQPPRPHPQMFTIDPAKGIISVLGTGLD
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                                                                                                                                                                                                                                                                                           ARRKVEKEPLLPPEDDMRDNV
                                                                                                                                                                                                                                                                                                                                 IRIKK-----DKGKDNV 819
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                                                                                                                                                                                                                                                                                                                                                                                                         -IVSLPVTFCSCVEG---SCFRPA----GHQTGIPTV-GMAVGILLTTLLVIGIILAVVF 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTYPFKAALEHGS-SNNWTV-EIRGQDELAMGLKKELEPGEYNIFVKLTDS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGIPDTTGTGTLLLLLQDVNDNGP--TPEPRSFEICS--RQPEKQILSIVDKD----LPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGGSSLSSVSEFHLILMDVNDNPPRLAKDYTGLFFCHPLSAPGSLIFEATDDDQHLFRGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAEDPDRDMRQKITYRMGSDPAGWLYIHPENGIVTATQPLDRESVHAINSTYKAIILAVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVFKAENPEPLVFGVKYNASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVAIGTKVGNV 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RETTPNYTLIVQATDQEGKGLSNTATAIIEVTDANDNIPIFNPTMYEG--VVEENKPGTE
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San Diego
California
                                   E: Campbell and
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                                                                                                                                 Barbara
                                                                                                                 T-Cadherin Adhesion
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                                     Village
                                                       Flores
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                                     Drive,
                                       Suite
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 30.4%; Pred. No. 2e-47; Matches 189; Conservative 104; Mismatches 261; Indels
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APPLICATION NUMBER: US 08/213,361
FILING DATE: 14-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/607,293
FILING DATE: 30-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (619) 535-9001
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                               757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 EVTEQLDREKIDRYTLLSHAVSASGQPVEDPMEIIITVMDQNDNKPVFIKEVFVGYIEEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 WKAPKPVEMVENSTDPHPIKITQVRWN---DPGAQYSLVDK--EKLPRFPFSIDQE-GDI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 VARLTVTDQDAPGSPAWQAVYHIKSGNLDGAFSIITDPSTNNGILKTAKGLDYETKSRYD
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REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/472,481 FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                        TAEDPDRDMRQKITYRMGSDPAGWLYIHPENGIVTATQPLDRESVHAINSTYKAIILAVD
                                                                                                                                                                                                                                                                                          TAKDPE---GLDISYSLRGDTRGWLKIDHVTGEIFSVAPLDREA----GSPYRVQVVATE 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RETTPNYTLIVQATDQEGKGLSNTATAIIEVTDANDNIPIFNPTMYEG--VVEENKPGTE:348
-IVSLPVTFCSCVEG---SCFRPA----GHOTGIPTV-GMAVGILLTTLLVIGIILAVVF 807
                                                                                                 H---FTFSLGSGSLQNDWEVSKINGTHARLSTRHTDFEERAYYVLIRINDGGRPPLEG-- 756
                                                                                                                                                              NGIPDTTGTGTLLLLQDVNDNGP--TPEPRSFEICS--RQPEKQILSIVDKD----LPP
                                                                                                                                                                                           VGGSSLSSVSEEHLILMDVNDNPPRLAKDYTGLFFCHPLSAPGSLIFEATDDDQHLFRGP 701
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                                                                      HTYPFKAALEHGS-SNNWTV-EIRGQDELAMGLKKELEPGEYNIFVKLTDS-----QGKA 630
                                                                                                                                                                                                                                                                                                                                                       LVVTVENKVPLSVPI---TLSTASVLVTVLDVNEPPVFVPPIKRVGVPEDLPVGQQVTSY 465
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                                                                           631 QVTQVKAQVCEC-EGTAKNCERRSYIVGG--LGVPAILGILGGIL---ALLILLLLLLLF 684
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Search completed: January 15, 2003, 08:20:03 Job time : 30.6438 secs

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Database
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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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249
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/laa/backfiles1.pep:*
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    DB
US-08-718-388-9
US-08-313-2888-18
US-07-971-096-4
US-08-175-096-4
US-08-175-096-4
US-08-434-418-6
US-08-174-739A-6
US-08-174-739A-6
US-08-196-37A-331
US-09-199-637A-331
US-09-429-516-1
US-09-429-516-1
US-09-429-516-3
US-09-249-697A-6
US-09-363-316B-24
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US-09-363-316B-24
US-09-363-316B-24
US-09-363-316B-24
US-09-363-316B-24
US-09-363-316B-24
US-09-363-316B-24
US-09-164-41A-39
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SWKRSSK : : AWRVPGS	ch 1 S		TELECOMMUNICATELEPHONE: TELEPHONE: TELEFAX: ('INFORMATION FOR	CLASSIFICATION ATTORNEY/AGENT NAME: MURPHY REGISTRATION REFERENCE/DOC	COMPUTER: I OPERATING SY SOFTWARE: P CURRENT APPLIC APPLICATION FILING DATE:	UNTRY: P: 220 OTER RE DIUM TY	ET:		-388-9 e 9, Ap No: 627 L INFOR		4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
SWKRSSKSTGLGDT : : AWRVPGSSKGCG	imilarity ; Conser	405 no a lin E:	(703) (703) (703) OR SEQ	CLASSIFICATION: TORNEY/AGENT INFO NAME: MURPHY JR, REGISTRATION NUMB REFERENCE/DOCKET	E. N. IB	USA DAB	NDENCE ADDRES SEE: BIRCH, PO BOX 747 FALLS CHURCH	: (MORIKAWA, : HARADA, N : NORTION: INVENTION: INVENTION: SEQUENCES:	388-9 9, Applicatio 0: 6271362 INFORMATION		19.9 119.9 119.9 119.9 119.7 119.7 119.7 119.3 119.3 119.3 119.3
TATREGCGP	22.18 41.48 vative	amino aci cid ear protein	TELEPHONE: (703) 205-8000 TELEPAX: (703) 205-8050 TELEPAX: (703) 205-8050 RMATION FOR SEQ ID NO: (9)	DN: 536 INFORMATION 7 JR, GERALD NUMBER: 28 PKET NUMBER:	COMPA PC-D In Rel DATA: R: US	FORM: oppy di	ESS , S 47 CH	PGA	ion US/08718388		367 367 367 367 367 110 110 110 290 290 290 369 455 33 33 31 31 31 31 31 31 31 31 31 31 31
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RESULT 3
US-07-971-096-4
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US-08-313-288B-18
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                                                                                                                                                                                                                                                                            Sequence 4, Application US/07971096 Patent No. 5480972 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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SEQUENCE CHARACTERISTICS:
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NAME: White, John P.
REGISTRATION UMBER: 28,678
REFERENCE/DOCKET NUMBER: 4002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                             APPLICANT: Singh, Mohan Bir
APPLICANT: Avjioglu, Asil
APPLICANT: Knox, Robert Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                            STREET: 60 51
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: Si
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OPERATING SYSTEM:
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OPERATING SYSTEM:
                                                                                 COUNTRY:
                                                                                                    STATE:
                                                                                                                                                ADDRESSEE:
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1185 Avenue of the Americas
                                                                               USA
                                                                                                                               60 State Street, Suite 510
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: January 5, 1995
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compatible
PC-DOS/MS-DOS
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Pred. No. 1
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-971-096-4
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US-08-175-096-4
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APPLICANT: Singh, Mohan Bir
APPLICANT: Avjioglu, Asil
APPLICANT: Knox, Robert Brue
TITLE OF INVENTION: ALLERGE
TITLE OF INVENTION: JOHNSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
               TELEFAX: (617) 227-59 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, SOFTWARE: Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC
TELECOMMUNICATION INFORMATION:
                              TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400 TELEFAX: (617) 227-5941
                                                                                                                                       APPLICATION NUMBER: US 07/971,096 FILING DATE: OCT 30, 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: LAHIVE & COCKFIELD
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NAME: Mandragouras Amv
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PRIOR APPLICATION DATA:
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STREET: U.
STREET: WA
                                                                                  NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-042 (IMI-022)
                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 263 amino acids TYPE: AMINO ACID TOPOLOGY: linear
                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Pred. No. 12;
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US-08-413-974-6
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity 35.3%;
Matches 12; Conservative
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                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                  TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/202,861
FILING DATE:
APPLICATION NUMBER: US/07/746,703
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 25
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                                                                                                                                                                                                                                                                                 NAME: Hohenschutz, Liza D. REGISTRATION NUMBER: 33,712 REFERENCE/DOCKET NUMBER: IMI
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CLASSIFICATION: 435
 48
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WY-----GKPTGAGPKDNGGACGYKDVDKAPFNG 76
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                                                                                                                                                                                    263 amino acids
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1 Liberty Place, 46th Floor
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Knox, Robert B.
Smith, Penelope
Avjioglu, Asil
                                                                                                                                                                                                                                   (215) 568-31
(215) 568-3949
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                                                              Conservative
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                                                                                                                                         protein
                                                                         21.5%;
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                                                                           Score 53.5;
Pred. No. 12;
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Pred. No. 12;
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RESULT 8
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US-08-433-288-6
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                                                                                                                                                                                                                                                                                                         US-08-433-288-6
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: IMI-051CNN1

CURRENT APPLICATION NUMBER: US/08/433,288

CURRENT FILING DATE: 1995-05-03

PRIOR APPLICATION NUMBER: 08/413,947

PRIOR FILING DATE: 1995-03-30

PRIOR FILING DATE: 1995-03-30

PRIOR APPLICATION NUMBER: 08/202,861

PRIOR FILING DATE: 1994-02-25

PRIOR APPLICATION NUMBER: 07/746,703

PRIOR FILING DATE: 1991-08-16
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                                                                               Sequence 6, Application US/08174739A Patent No. 6265566
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NUMBER OF SEQ ID NOS: 25
                                               GENERAL INFORMATION: APPLICANT: Singh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: FILE REFERENCE: IMI
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1990-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: FILE REFERENCE: IM
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                     LENGTH: 263
TYPE: PRT
ORGANISM: LOLium perenne
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                                                                                                                                                                                                                                                           Local
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al Similarity 35.3%;
12; Conservative
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12; Conserv
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PatentIn Ver. 2.0
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Singh, Mohan Bir
Knox, Robert B.
Smith, Penelope
Avjioglu, Asil
                                                                                                                                                                                                                                          Conservative
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    Mismatches

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Pred. No. 12;
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Pred. No. 12;
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APPLICANT: APPLICANT: APPLICANT:

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US-08-434-256-6
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Patent No. 6451324
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir, Knox, Robert B., Smith, Penelope,
APPLICANT: Ayjioglu, Asil, Theerakulpisut, Piyada, Hough, Terryn
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,256
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6451324ris
STREET: 1 Liberty Place, 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: IM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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APPLICANT: Hough, Terryn
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                                                                                                                                                                                                                                                                                                   STREET: 1 Liberty : CITY: Philadelphia
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CITY: Boston
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REFERENCE/DOCKET NUMBER:
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12; Conserv
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amino acid
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                                                                                                                                                                                                                                                                       USA
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IMPH-0003
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Pred. No. 12;
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; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-331
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Best Local Similarity
Tatches 17; Conserv
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Patent No. 633...
Patent INFORMATION:
                                                                                                                                                                                                          GENERAL
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SEQ ID NO 331
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APPLICANT: Magna, Holly
APPLICANT: Schäffer, Paul
APPLICANT: Schäffer, Paul
APPLICANT: Mitchael
APPLICANT: Mitchael
APPLICANT: Mitchell, Peter
APPLICANT: Hutchinson, Nancy
APPLICANT: Hutchinson, Nancy
APPLICANT: HUXBYTION: HUMAN NUCLEOTIDE PYROPHOSPHOHYDROLASE-2
FILE REFERENCE: PF-0420 US
CURRENT APPLICATION NUMBER: US/08/996,083A
CURRENT FILING DATE: 1997-12-22
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USBS THEREOF
FILE REFERENCE: 00786/361002
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APPLICANT:
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LENGTH: 263 amino acids
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                                                                                                                                                                                                                                                                                                                                       552 SKGTGLGLYLSRELCESNQARIDYRNREEGGGC---FRITFAHPRK 594
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Local Similarity 35.3%;
les 12; Conservative
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                                                                                                                                                                                                          INFORMATION:
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Rahme, Laurence G.
Mahajan-Miklos, Shalina
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Pred. No. 12;
1; Mismatches
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Pred. No. 3;
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US-09-429-516-1
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 3
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature OTHER INFORMATION: Incyte Clone No. 6124095: 1388013 PUBLICATION INFORMATION:
                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                    NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                     IMMEDIATE SOURCE:
SATPE1008
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                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hutchinson, Nancy
APPLICANT: MUTTY, LYNN E.
TITLE OF INVENTION: HUMAN NUCLEOTIDE PYROPHOS
TITLE OF INVENTION: PHOHYDROLASE-2
                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
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 LIBRARY: SALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 WGPWGPCSGSCGPGRRLRRRHCPSPAGDACP--GRPLEAQKCVRPR 195
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                                                                          TYPE: amino aci
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                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                         ENGTH:
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Pred. No.
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86;
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US-09-429-516-3
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Best Local Similarity 34.8
Matches 16; Conservative
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                                                        Matches
                                                                       Best
                                                                                  Query Match
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/429,516
                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
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APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN NUCLEOTI
TITLE OF INVENTION: PHOHYDROLASE-2
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152
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ZIP: 943
                                                                                                                            LIBRARY: SATPI
CLONE: 422069
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                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                      Local
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                         2 WYSWKRSSKSTGLGDTATREGCGPSQSDGCPYNGR----LTTVKPR 43
WGPWGPCSGSCGPGRRLRRRHCPSPAGDACP--GRPLEAQKCVRPR 195
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5, 6251389
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                                                                    Similarity
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Schaffer, Paul
Lawton, Michael
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                                                        Conservative
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                                                                    Score 53;
Pred. No.
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Pred. No.
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                                                     red. No. 86;
Mismatches 23
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                                                                                   Length 1156;
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RESULT 14

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APPLICANT: Young, George
TITLE OF INVENTION: LOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL
TITLE OF INVENTION: LIVER SPLEEN

FILE REFERENCE: 24011-727
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 08/968,800
PRIOR FILING DATE: 1997-11-22
NUMBER OF SEQ ID NOS: 1997-11-22
NUMBER OF SEQ ID NOS: 197E: PRT
ORGANISM: Homo sapiens
FEATURE: NAME/KEY: VARIANT
LOCATION: (1)...(553)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-249-697A-6
Search completed: January 15, 2003, 08:19:58 Job time: 3.35616 secs
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                                                                                                                                                                                                                                                            ; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-249-697A-19
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US-09-249-697A-19
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                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ford, John
APPLICANT: Yeung, George
APPLICANT: Yeung, George
TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL
TITLE OF INVENTION: LIVER SPLEEN
FILE REFERENCE: 24011-727
CURRENT APPLICATION NUMBER: US/09/249,697A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 08/968,800
PRIOR APPLICATION NUMBER: US 08/968,800
PRIOR FILING DATE: 1997-11-22
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 19
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/09249697A Patent No. 6392018
GENERAL INFORMATION:
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                                                                                                                                                                         Query Match 20.9%;
Best Local Similarity 29.1%;
Matches 16; Conservative
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Best Local Similarity 29.1%;
Matches 16; Conservative
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                                                                                   51 YGWRRNSK--GVCEATCEPGCKFGECVGPNKCRCFPGYTGKTCSQDVNECGMKPR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 YGWRRNSK--GVCEATCEPGCKFGECVGPNKCRCFPGYTGKTCSQDVNECGMKPR 103
                                                                                                            3 YSWKRSSKSTGLGDTATREGC-----GPSQSDGCP-YNGRLTT------VKPR 43
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                                                                                                                                                                                             Score 52; DB 4; Length 553; Pred. No. 49;
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Minimum DB
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No.
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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2000
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Match
  100.0
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26.1
25.1
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249
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Listing first 45 su
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    2122222220
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             AAW74045
AAB58866
AAB638135
AAW99302
AAW99301
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AAB63063
AAR07289
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             Human secreted pro
Human BAI2 protein
Drosophila melanog
Circumsporozoite a
                                                                Human D2H binding
Drosophila melanog
Amino acid sequenc
Human BAI3 protein
                                                                                                                                                      Description
                                                                                                                          Human HPT-1 bindin
human diagno
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AAW74068
 Alvarez VL,
Omahony DJ,
WPI; 1999-009568/01
                                                                                                             15-MAY-1997;
                                                                                                                                         15-MAY-1998;
                                                                                                                                                                     19-NOV-1998
                                                                                                                                                                                                W09851325-A2
                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      04-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                 AAW74068;
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	12 AAR13175				22 AAM9458																	23 AAB47770											AAW863	
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NS181RLFAuth plasm	1-RLfdelta	-Fc bindin	Human colon cancer	Human polypeptide	_	Human thrombospond	Human MOL4 protein	Human semaphorin G	Human semaphorin G	Human semaphorin G	Human semaphorin G	semaphori	Human semaphorin G	Human secreted pro	semaphori		Novel human diagno	Drosophila melanog		=		_	3	l human	•	colon c	_	_	Mouse thrombospond	e thromb	l human	human diagn	y injur	Amino acid sequenc

ALIGNMENTS

Gastro-intestinal transport receptor; binding protein; hSI; HPT1; D2H; hpEPT1; human; GI tract receptor; sucrose-isomaltase complex; intestinal peptide-associated transporter; hypertension; diabetes; osteoporosis; haemophilla; anaemia; cancer; migraine; angina pectoris; therapeutic agent delivery; therapy. (CYTO-) CYTOGEN CORP. (ELAN-) ELAN CORP PLC. Human HPT-1 binding protein HAX35 (first entry) Belinka BA, (Patterson CA, 97US-0046595 98WO-US10088 Cagney GM, Singleton Carter JM, J; Lambkin

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ARESULT 2
AAW74045
ID AAW7
XX AAW7
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XX Gast
KW D2H;
KW D2H;
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                                                                                                           Alvarez
Omahony
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gastro-intestinal transport receptor; binding protein; hSI; HPT1; D2H; hPEPT1; human; GI tract receptor; sucrose isomaltase complex; intestinal peptide-associated transporter; hypertension; diabetes; osteoporosis; haemophilia; anaemia; cancer; migraine; angina pecto;
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  New proteins
                                                        WPI; 1999-009568/01.
                                                                                                                                                                                                                                                                             15-MAY-1997;
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                                                                                                                                                                                             (ELAN-)
                                                                                                                                                                                                                       (CYTO-)
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  that bind
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                                                                                                           Belinka BA, (
Patterson CA,
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                                                                                                                                                                                                                                                                                                                                   98WO-US10088
                                                                                                                                                                                           PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  delivery; therapy.
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specifically to
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Singleton
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Pred. No. 1.2e-26;
Mismatches 0;
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receptors
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                                                                                                                                                                                         CC D2H protein. The invention relates to purified proteins (1) that bind CC specifically to at least one of the gastro-intestinal (GI) tract CC receptors human intestinal peptide-associated transporter (HPT1).

CC hPEPT1, D2H and human sucrose-isomaltase complex (hSI). (I) provide CC active transport of therapeutic agents through human and animal GI tissue CC (into the blood) for in vivo delivery, particularly for treatment or CC prevention of hypertension, diabetes, osteoporosis, haemophilia, anaemia, CC cancer, migraine, or angina pectoris. Specifically they are used to CC deliver insulin or leuprolide, but many other suitable therapeutic agents CC and antigens. (I) may also provide targeting to the GI tract. Other uses of (I) are: (i) to determine the level of specified receptors in a sample CC (in a binding assay); and (ii) to screen for molecules that bind (I). CC Immunogenic analogues or derivatives of (I) are used to raise antibodies and in immunoassays. The antibodies are used to locate, detect and CC measure (I), e.g. for imaging, monitoring treatment, tissue analysis CC etc., also for peptide purification and immobilisation.
                                                                                                Query Match
Best Local
                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gastro-intestinal tract and related nucleic acid - chimaeras antibodies, used to deliver therapeutic or diagnostic agents through, the gastrointestinal tract, e.g. insulin or leuprol
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2;
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                                       N
WSSWNWSSKTTRLGDRATREGCGPSQSDGCPYNGRLTTVKPR
                                       WYSWKRSSKSTGLGDTATREGCGPSQSDGCPYNGRLTTVKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents a peptide
                                                                                                Similarity
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                                                                                                                                                          44
                                                                               Conservative
                                                                                                                                                            Ą,
                                                                                                80.3%;
                                                                             1;
                                                                                                Score 200;
Pred. No. 5
                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that specifically binds to the
                                                                                                DB 20;
.8e-20;
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  43
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                                                                                                                  Length
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                                                                                                                      44;
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RESULT 3
ABB58866
WPI; 2001-656860/75
                          Venter JC,
                                                    (PEKE ) PE
                                                                              23-MAR-2000;
11-JUL-2000;
                                                                                                                    23-MAR-2001;
                                                                                                                                             27-SEP-2001
                                                                                                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                                       pharmaceutical.
                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling;
                                                                                                                                                                                                                                                               Drosophila
                                                                                                                                                                                                                                                                                                                   ABB58866;
                                                                                                                                                                                                                                                                                                                                         ABB58866 standard; Protein; 793 AA
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                                                    CORP NY.
                                                                                                                                                                                                                                                             melanogaster
                          Adams
                                                                                                                                                                                                                                                                                       (first entry)
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                                                                              2000US-191637P
2000US-0614150
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                                                                                                                                                                                                                                                           polypeptide
                          PWD,
                         Myers
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                                                                                                                                                                                                                                                               ID NO
                                                                                                                                                                                                                                                               3390
                                                                                                                                                                                                                                     insecticide;
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New isolated nucleic a

acid a and

detection reagent for detecting for elucidating cell signalling

1000 or more

interactions

N-PSDB;

ABL02969

Disclosure;

SEQ

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3390;

21pp

Sequence Listing; English

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RESULT 4
AAB08135
ID AAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Type 1 repeat; thrombospondin-1; TSP-1; Type I repeat peptide; TRP; KIAA0588; KIAA0550; anglogenesis inhibitory protein; anglogenesis; cancer; tumour; rheumatoid arthritis; psoriasis; retinopathy; ocular anglogenic disease; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasis; rubeosis; osler-Webber Syndrome; myocardial anglogenesis; haemophiliac joint; plaque neovascularisation; telanglectasia; anglofibroma; wound granulation; coronary collateral; cerebral collateral; arteriovenous malformation; ischemic limb anglogenesis; neovascular glaucoma; retrolental fibroplasia; fracture; vasculogenesis; heliobacter related disease; hematopolesis; ovulation; menstruation; placentation; birth control; embryo implantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL01847-ABBR72072).
                                                                                                                                                                                             WPI;
          The present sequence represents a KIAA0550 polypeptide. The specification describes a non-naturally occurring Type I repeat peptide (TRP), derived from human thrombospondin-1 (hTSP-1), KIAA0688 or KIAA0550 proteins. The TRP protein is an anglogenesis inhibitory protein. TRP
                                                                                                                                                                                                                                                                                                                                                                                                                      НОПО
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                               Claim
                                                                                                                                            Non-naturally occurring Type I repeat peptide (TRP) derived from thrombospondin-1, KIAA0688 or KIAA0550 proteins, useful in the
                                                                                                                                                                                                                           Mazarakis N,
                                                                                                                                                                                                                                                         (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                         15-FEB-1999;
                                                                                                                                                                                                                                                                                                                        15-FEB-2000; 2000WO-GB00520
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protein
for the
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is an angiogenesis treatment of condit
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Pred. No. 2.1;
10; Mismatches
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'
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2.1;
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350

EWSPWSLCSFTCGRGQRTRTRSCTPPQYGGRPCEGPETHHKP 391 EWYSWKRSSKSTGLGDTATREGCGPSQSDGCPYNGRLTTVKP 42 Matches Query Match Best Local

Local

l Similarity 15; Conserv

Conservative

26.1%; 35.7%;

Pred. No. 12; l; Mismatches Score No.;

26;

Indels

0

Gaps

0

DB 12; 20;

Length 1522;

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RESULT 5
AAW99302
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angiogenesis and cancer. Angiogenic mediated diseases include tumours, rheumatoid arthritis, psoriasis, ocular angiogenic diseases, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis), Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischemic limb angiogenesis, neovascular glaucoma, retrolental fibroplasia, heliobacter related diseases, fractures, vasculogenesis, hematopoiesis, ovulation, menstruation and placentation. TRPs are also useful in the treatment of disease of excessive or abnormal stimulation of endothelial cells. TRP can also be used as a birth control agent, as
                           This sequence represents the human BAI3 protein. The gene is expressed specifically in the brain and plays an important role in cancer formation the brain. The BAI3 protein can be used in drug compositions to diagnose, prevent or treat such cancers.
Sequence
                                                                                                  Claim
                                                                                                                               cancer formation
                                                                                                                                                                        WPI; 1999-183823/16.
N-PSDB; AAX21357.
                                                                                                                                                                                                                                                                                                         09-FEB-1999
                                                                                                                                                                                                                                                                                                                                      JP11032766-A
                                                                                                                                                                                                                                                                                                                                                                                            Human; BAI3; brain; cancer; drug; diagnosis; prevention; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                         Human BAI3 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                             New human BAI gene
                                                                                                                                                                                                                  (SAKA ) OTSUKA PHARM
                                                                                                                                                                                                                                               23-MAY-1997;
                                                                                                                                                                                                                                                                            16-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  it prevents the vascularisation required for embryo implantation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EWYSWKRSSKSTGLGDTATREGCGPSQSDGCPYNGRLTTVKP 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
15; Conser
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1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 AA;
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                                                                                                  26-30;
                                                                                                                                                                                                                                                 97JP-0150460
                                                                                                                                                                                                                                                                            97JP-0176485
A
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35.7%;
                                                                                                                                                                                                                    ၀
                                                                                                 62pp;
                                                                                                                                             is expressed
                                                                                                 Japanese.
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                                                                                                                                             in
                                                                                                                                             brain
                                                                                                                                             plays important role
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RESULT 6
AAB23601
В
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Best Local S
Matches 15
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17-AUG-1999;
23-SEP-1999;
01-OCT-1999;
29-NOV-1999;
29-NOV-1999;
                                                                                                             The present sequence is the sequence of a human secreted protein. Its CDNA was isolated from a foetal brain cDNA library. The proteins and coding sequences of the invention can be used in the isolation of similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have uses as nutritional supplements, as cytokine or cell proliferation factors, in immune modulation, where they may be used to treat immune and autoimmune diseases, as haematopolesis regulators (treating myeloid or lymphoid cell deficiencies), in the promotion of tissue growth, they may have chemokine or chemotactic activity, haemostatic or thrombolytic activity, or anti-inflammatory activity.
                                                                                           Sequence
                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                              New secreted proteins and polynucleotides encoding them, which are derived from Homo sapiens, useful for therapy, diagnosis, and research, as well as nutritional sources or supplements -
                                                                                                                                                                                                                                                                                                                               N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                Valenzuela D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nutritional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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EWSPWSLCSFTCGRGQRTRTRSCTPPQYGGRPCEGPETHHKP
                     EWYSWKRSSKSTGLGDTATREGCGPSQSDGCPYNGRLTTVKP 42
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                                                                                                                                                                                                                                                           9; Page 234-238;
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                                             . Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        ALPHAGENE
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990S-0149639
990S-0155686
990S-0157247
990S-0167823
990S-0167823
20000S-0298733
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                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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pplement; immune modulation; autoimmune disorder;
regulation; tissue growth; haemostasis; inflammation.
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16..1522
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                                                      26.1%;
35.7%;
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                                           Score 65; DB Pred. No. 12; 1; Mismatches
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                                                                                                                                                                                                                                                          English.
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                                                     DB
. 12;
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                                                                21;
                                             26;
                                                                                                                                                                                                                                                                                                                                                                Rapiejko
 391
                                                                   Length 1522;
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                                           Gaps
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RESULT 7
AAW99301
ID AAW9
XX AAW9
XX AAW9
XX AAW9
XX Huma
XX Huma
XX Homc
XX JP11
XX JP11
XX 16-C
XX SPE (SAP
XX WP1
DR WP1
DR WP1
XX NEW
PT CANC
XX Clai
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XX Sequ
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ABB63063
PXRRX FXX
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the human BAI2 protein. The gene is expressed specifically in the brain and plays an important role in cancer formation the brain. The BAI2 protein can be used in drug compositions to
                 23-MAR-2000;
11-JUL-2000;
                                                                                                                            Drosophila; dev pharmaceutical.
                                                                                                                                                         Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       New human BAI gene cancer formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; BAI2; brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW99301 standard;
                                               23-MAR-2001; 2001WO-US09231
                                                                  27-SEP-2001
                                                                                      WO200171042-A2
                                                                                                         Drosophila melanogaster.
                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                   ABB63063 standard;
                                                                                                                                                                                                                                                                                                                                                                  diagnose,
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX21356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-183823/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SAKA ) OTSUKA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP11032766-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW99301;
                                                                                                                                                                                                                                                                   357
                                                                                                                                                                                                                                                                                     1 EWYSWKRSSKSTGLGDTATREGCGPSQSDG------
                                                                                                                                                                                                                                                                   EWGSWSLCSRSCGRGSRSRMRTCVPPQHGGKACEGPELQTKLCSMAACPVEGQ 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   2:
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                                                                                                                                                                                                                                                                                                       l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                 Page
                                                                                                                                                                                                                                                                                                                                                                  prevent or
                                                                                                                                                                                                                                                                                                                                              1572 AA;
                                                                                                                                     developmental
                                                                                                                                                                                                                                                                                                         Conservative
                  2000US-191637P
2000US-0614150
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                  22-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                  25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; drug; diagnosis; prevention; treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                 62pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ၀
                                                                                                                                                                                                                                                                                                                                                                   treat such cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed in
                                                                                                                                     biology;
                                                                                                                                                                                                                                                                                                                                                                                                                  Japanese.
                                                                                                                                                                                                                                                                                                        Score 64.5; Di
Pred. No. 15;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                      cell signalling; insecticide;
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(PEKE) PE CORP NY

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RESULT 9
AARO7289
ID AARO7289
XX AARC
XX AARC
XX CARC
XX CS
XX CS
XX CS
XX CS
XX CS
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XX I
PN EP
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Best Local Similarity
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The protein was produced by expression of a synthetic gene. analogue comprises AAs 43-123 of the native p. falciparum of protein, followed by four repeat sequences (three "B"s, i.e
                                                                                                          Claim 10; Fig 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CS protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Circumsporozoite analogue Falciparum 3.
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                   Recombinant plasmodium circumsporozoite analogues - lacking one or more repeat epitope(s) for use as a malaria sub-unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP392820-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75
N-PSDB; ABL07166.
                                                                                                                                                                                                                                                                   N-PSDB; AAQ06152.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-1990
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                                                                                                                                                                                                                                                                                                                                           Bathurst IC,
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                                                                                                        22pp; English.
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a and
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                                                                                                                                                                                                                                                                                                                                              Gibson
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Pred. No. 10;
4; Mismatches
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                                                                                          polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique; to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and one "A", i.e. NVDP), followed by AAs 289-374 of the native protein. Reduction of the immunological dominance of the repeat relative to the epitopes in the regions flanking the repeats enhances sporozoite neutralising activity.

See also AAR07287-91.
The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                              Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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DB; AAS84301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome mapping; gene mapping; gene therapy; forensic
upplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                              SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184
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2000US-0649167
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                                                                                                                                                                                                                                                                                                           50473; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang
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Pred. No. 7.4;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                           of mutations to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184;
                                                                                                                                                                                                                                               chromosome
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RESULT 11
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                                             Query Match
Best Local
                                    Matches
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                                                                                                                                                                                                                                                                                                                                           11-JAN-2000;
17-FEB-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                         Ota T,
                                                                                                 The present sequence represents a thrombospondin 1-like (TSP1-like) protein. The cDNA sequence encoding human TSP1-like protein was isola from a human 10 week-aged foetal tissue cDNA library. The TSP1-like protein may be involved in intracellular vesicle transport. Secretion of the TSP1-like protein is reduced in brain tumours. It can be used in the screening of target compounds, and is useful for diagnosis, prediction and treatment of brain tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                              Yano
                                                                             Sequence
                                                                                                                                                                                        Claim 2; Page 72-80; 105pp; Japanese.
                                                                                                                                                                                                                           Gene
                                                                                                                                                                                                                                                                                                                       (HELI-)
                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1999;
27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombospondin 1-like protein; TSP1-like protein;
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EWYSWKRSSKSTGLGDTATREGCG--PSQSDGCPYNGR-----LTTVKP 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WHSWRQQGWGAHLGSSATGPGC-----XQGRPTCV
                                                                                                                                                                                                             encoding thrombospondin-like protein, bodies to it, useful for diagnosis and
                                                                                                                                                                                                                                               2001-541222/60.
)B; AAH77754.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumour
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                                             Similarity
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Kanzaki K,
                                                                                                                                                                                                                                                                                                 Isogai T,
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                                                                             1068 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                                                                                                                                                                           99JP-0248036.
99JP-0300253.
99US-0159590.
2000JP-0118776.
2000US-0183322.
2000JP-0183767.
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                                   Conservative
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                                                                                                                                                                                                                                                                                                                       INST.
                                                                                                                                                                                                                                                                             Nishikawa T, I
n T, Wakamatsu .
(, Inoue Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of.
                                            23.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            murine thrombospondin 1-like protein.
                                 Score 58.5; D
Pred. No. 61;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
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Pred. No. 38;
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                                                                                                                                                                                                                                                                                       Hayashi K,
A, Nagai K,
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                                                        DB
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                                                                                                                                                                                                              and the protein and
treatment of brain
                                                                                                                                                                                                                                                                                       Saito K,
(, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
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                                  21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vesicle transport;
                                  Indels
                                                        Length 1068;
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                                                                                                                                                                                                             of brain
                                                                                                                                                                                                                                                                                      Yamamoto J;
T, Murakami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  710;
                                                                                                                                   Secretion
                                  7;
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                                                                                                                                                                                                               tumours
                                 Gaps
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                                                                                                                                                        isolated
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Qy

RSSKSTGLGDTA-TREGC-----GPSQSDGCPYNGRLTTVKPRK

Matches Query Match Best Local

Similarity

23.3%;

Conservative

ω ,.

Score 58; DB Pred. No. 11; 3; Mismatches

Length 226

Indels

9

Gaps

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RESULT 12
AAW86332
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                                                                                               The present sequence represents a kidney injury associated molecule (CC (KIM) protein. KIM proteins can be administered therapeutically CC by expressing KIM encoding polynucleotides, to promote growth and/or CC survival of damaged tissue (e.g. renal tissue), since the KIM proteins CC survival of damaged tissue (e.g. renal tissue), since the KIM proteins CC KIM fusion proteins, conjugates, antibodies and vectors can also be used CC KIM fusion proteins, conjugates, antibodies and vectors can also be used CC KIM fusion proteins, conjugates, antibodies and vectors can also be used CC therapeutically, e.g. these or the KIM proteins may be included with an acceptable carrier in pharmaceutical compositions, useful for therapy/ crophylaxis of conditions associated with disfunction/disregulation of CC KIM genes or proteins, especially renal diseases or impairments of renal function in humans (e.g. acute renal diseases or impairments of renal function in humans (e.g. acute renal failure, acute nephritis). The cc polynucleotides can be used to produce antisense sequences which, when CC internalised into cells, can disrupt expression of a cellular KIM gene, as on the proteins and polynucleotides are cuseful diagnostically e.g. to block the growth of tumours dependent on CC KIM for growth) or compositions. The proteins and polynucleotides are cuseful diagnostically e.g. to detect and quantify renal injury or impaired confunction), or abnormal responses to tissue injury (indicative of increased risk, or presence of, renal injury (indicative of increased risk, or presence of, an autoimmune response or abnormal can calso be used to locate KIM-producing cells (especially specific local).
                                                             e.g. tissue masses abnormally producing/expressing KIM such as tumours arising from/affecting renal tissue), by contacting cells with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kidney injury associated molecule; kidney injury related mol KIM; tissue growth promotion; regeneration; renal condition; acute renal failure; acute nephritis; tumour.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 168; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kidney injury-associated molecule, KIM, polypeptides - upregulated in injured or regenerating tissues, useful to promote tissue growth
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                                        imageable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and regeneration, especially to treat renal conditions
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23-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kidney injury associated molecule HW088 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 EWSFWEDCSRSCGHGNQTRTRTCSNPPAQHGGRPCEGHAVETIMCNIRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein; 226
                                        KIM-binding reagent and
226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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97US-0047490.
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                                        reagent accumulation
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RSGLRTALAPRALTPQVCSPFATGPRQSDGTLYEFRTYSLKPSK 56

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                                                                                                                                                      The invention relates to isolated polynucleotide (I) and CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical considered involving partners are useful for treating CC diagnost of sites expressing (II). (I) and (II) are useful for treating CC diagnostics, forensics, gene mapping, identification of mutations in CC diagnostics forensics, gene mapping, identification of mutations in CC diagnostics forensics gene mapping, identification of mutations (I) and products dependent on DNA and CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this pattent did not appear in the printed CC at fits. Wipo.int/pub/published_pct_sequences.
                                                               Query Match
Best Local Similarity
Matches 14; Conser
                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID No 35520; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to assemble disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT,
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forension supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002
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 133
                              4
SWQGTSCGGG-----TSGCGRLQXDGVASRGRWDPARPRE 167
                              SWKRSSKSTGLGDTATREGCGPSQSDGCPYNGRLTTVKPRK 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-639362/73.
                                                                                                                              244
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                              23.3%;
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                                                                              Score
Pred.
                                                               Mismatches
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                                                                                            22;
                                                             17;
                                                                                            Length 244;
                                                               Indels
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                                                             Gaps
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RESULT 14
ABG16825
ID ABG16
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CC Note: The sequence data for this patent did not appear in the printed construction. Int/pub/published_pct_sequences.
                                                                                                                 Matches
                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 47184; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #16816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS81012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631
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19
WRSPCCPAPKTGAWASATQGGC-PGPSSSCPASSR--SVSPR 57
                                                    WYSWKRSSKSTGLGDTATREGCGPSQSDGCPYNGRLTTVKPR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-639362/73.
                                                                                                                                                Similarity
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                                                                                                              Conservative
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                                                                                                                                             23.1%;
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                                                                                                                                          Score 57.5;
Pred. No. 6
                                                                                                              Mismatches
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                                                                                                                                                                           DB
                                                                                                              18;
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                                                                                                                                                                     Length
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RESULT 15
AAU74796
ID AAU74
XX AAU74
XX AAU74
XX AAU74
XX AAU74
XX DAY AAU74
XX DAY AAU74
XX DAY AAU74
XX Throm
KW Throm
KW Throm
KW PLLIG
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KW POOLE
KW POOLE
FT POOLE
                                                                                                                                                                                                                                                                                     the tumour); for decreasing proliferation of tumour cells; in the treatment of diseases and conditions associated with angiogenic activity or misregulated growth and angiogenesis mediated diseases such as cancer, solid tumour, tumour metastasis, benign tumour, (e.g. haemangioma, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas), rheumatoid arthritis, psoriasis, ocular angiogenic diseases (e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vulnerary; neovascularisation; cell proliferation inhibitor; cancer; solid tumour; haemangioma; acoustic neuromas; neurofibroma; trachoma; pyogenic granulomas; rheumatoid arthritis; ocular angiogenic disease; retinopathy; psoriasis; macular degeneration; corneal graft rejection;
                          telanglectasia, plaque neovascularisation, haemophiliac joints, angiofibroma or wound granulation. The composition induces apoptosis and inhibits neovascularisation in the tumour cells. This amino acid sequence represents a recombinant protein, 3TSR, derived from mouse thrombospondin-2 (TSP-2) and containing the 3 type 1 repeat (TSR) regions of TSP-2, described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neovascular glaucoma; retrolental fibroplasia; rebeosis; angiofibroma; Osler-Webber syndrome; myocardial angiogenesis; haemophiliac joints; plague neovascularisation; telanglectasia; wound granulation;
                                                                                                                                                                                                                                                    diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for killing cancerous cells (preferably tumour); for reducing volume or inhibiting growth of a tumour (inhibiting neovascularisation the tumour); for decreasing proliferation of tumour cells; in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of human thrombospondin-1 (TSP -1), a type 1 repeat polypeptide and potent inhibitor of tumour growth and anglogenesis. The composition is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition useful for treatment of cancer comprises cDNA encoding amino acids of human thrombospondin-1 or its conservative variant and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apoptosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse thrombospondin-2 (TSP-2) derived recombinant protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a composition comprising cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000;
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                                                                                                                                                                                                                            rebeosis), Osler-Webber syndrome, myocardial angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page -; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carrier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-106273/14.
   This sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Vector_derived_peptide
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not appear in the specification but has been
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                                                                                                                Query Match
                                                                                                                                                               created using the mouse thrombospondin-2 (TSP-2) wild type sequence (see AAU74786) from information given in the invention.
                                                                                                                                         Sequence
127 P 127
                       42 P
                                            68 WSPWSSCSVTCGVGN-VTRIRLCNSPVPQMGGKNCKGSGRETKPCQRDPCPIDGRWSPWS 126
                                                                                                      Local
                                                                   2 WYSWKRSSKSTGLGDTATR-------EGCG----PSQSDGCPYNGRLTTVK 41
                       42
                                                                                           l Similarity 27. 17; Conservative
                                                                                                                                          183 AA;
                                                                                                      23.1%;
                                                                                           6,
                                                                                                      Score 57.5;
Pred. No. 1
                                                                                           Mismatches
                                                                                                         <u>;</u>
                                                                                                                  DΒ
                                                                                           17;
                                                                                                                  23;
                                                                                            Indels
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                                                                                                                  183;
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Search completed: January 15, 2003, 08:17:06 Job time: 7.31507 secs

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                      Score
 seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                January 15, 2003, 08:16:02 ; Search time 9.09132 Seconds (without alignments) 96.208 Million cell updates/sec
                                                                                                                                                                                                                                                                                Query
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                                                                                                                                                                                                                                                                    Match
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113.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/FOT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
EWYSWKRSSKSTGLGDTATR.....PSQSDGCPYNGRLTTVKPRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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 469
939
954
1078
11078
11093
11093
11136
11151
1188
1588
1588
1588
8000
8000
877
 0 US-09-925-301-1279
0 US-09-854-845-16
0 US-09-854-845-6
0 US-09-854-845-2
0 US-09-854-845-2
0 US-09-854-845-12
0 US-09-854-845-12
0 US-09-854-845-12
0 US-09-854-845-12
0 US-10-025-380-1116
0 US-10-025-380-1116
0 US-10-01-857-127
0 US-10-001-857-127
0 US-09-764-864-1174
0 US-09-764-853-800
0 US-09-764-898-200
0 US-09-764-898-200
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Compugen Ltd.
        Sequence 1279, Ap
Sequence 16, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 17, Appli
Sequence 110, Appl
Sequence 1116, Ap
Sequence 1116, Ap
Sequence 1116, Ap
Sequence 1117, Ap
Sequence 1174, Ap
Sequence 272, Appli
Sequence 273, Appli
Sequence 273, Appli
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19.5	19.5	19.5	19.5	19.5	19.5	19.5	19.7	19.7	19.7	19.7	19.7	19.9	20.1	20.3	20.7	20.7	20.9	20.9	20.9	20.9	20.9	20.9	20.9	20.9	20.9
499	499	278	277	267	258	211	2491	849	849	459	459	147	81	48	178	52	559	554	554	553	553	338	338	338	338
10	10	9	10	10	9	9	9	10	10	10	9	9	10	10	10	9	10	10	10	10	10	9	9	9	9
US-09-735-171A-2	US-09-735-169A-2	US-09-731-449-25	US-09-864-761-46564	US-09-853-386-106	US-09-731-449-28	US-09-731-449-29	US-10-000-789-2	15	US-09-752-639-152	US-09-741-152-2	US-10-195-517-2	US-10-016-634A-115	US-09-764-860-399	US-09-864-761-42865	US-09-764-853-469	US-09-796-692-1529	US-09-981-649A-28	US-09-981-649A-32	US-09-981-649A-30	US-09-981-649A-24	US-09-981-649A-6	US-09-978-189-119	US-09-999-832A-119	-09-97	US-09-978-697-119
Sequence 2, Appli		Sequence 25, Appl	Sequence 46564, A	Sequence 106, App	Sequence 28, Appl	Sequence 29, Appl	` ₽	Sequence 152, App	Sequence 152, App	Sequence 2, Appli	Sequence 2, Appli	Sequence 115, App	Sequence 399, App	Sequence 42865, A		Sequence 1529, Ap	Sequence 28, Appl	Sequence 32, Appl	Sequence 30, Appl	24,	e 6, 🗜	•	119,	Sequence 119, App	•

ALIGNMENTS

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RESULT 2
US-09-854-845-16
; Sequence 16, Application US/09854845
; Patent No. US20020098491A1
                                                                                                                                                                                                                                                              NAME/KEY: SITE

LOCATION: (15)

TOTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (81)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1279
                                                                                                                     В
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US-09-925-301-1279
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Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
                                                                                                                                                                                              Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1279
LENGTH: 469
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                     78
                                                                                                                                                    4 SWKRSSKSTGLGDTATREGCGPSQSDGCP 32
                                                                                                                     AWRXPGSSKGCG----EGCGP---QGCP
                                                                                                                                                                                              l Similarity 41.4
                                                                                                                                                                                                             22.9%;
                                                                                                                                                                                            Score 57; DB Pred. No. 11; 2; Mismatches
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                                                                                                                                                                                                             DB 10; Length 469, 11;
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PRIOR APPLICATION NUMBER: US 60/208,893
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 50
SOETWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 954
TYPE: PRT
ORGANISM: homo sapiens
US-09-854-845-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT ; ORGANISM: homo sapiens US-09-854-845-16
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APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: TINENCE: LEX-0177-USA
CURRENT APPLICATION NUMBER: US/09/854,845
CURRENT APPLICATION NUMBER: US/09/854,845
CURRENT APPLICATION NUMBER: US 60/205,274
PRIOR APPLICATION NUMBER: US 60/205,274
PRIOR APPLICATION NUMBER: US 60/208,893
PRIOR APPLICATION NUMBER: US 60/208,893
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 50
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
                                                                                     GENERAL INFORMATION:
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                                                                                                       Sequence 6, Application US/09854845 Patent No. US20020098491A1
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Best Local
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  APPLICANT: Walke, D. Wade
APPLICANT: Wang, Xiaoming
APPLICANT: Scoville, Johr
APPLICANT: Turner, C. Ale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Walke, D. Wade
APPLICANT: Wang, Xiaoming
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020098491A1el Human Semaphorin Homologs and Polynucleotic FILE REFERENCE: LEX-0177-USA
CURRENT APPLICATION NUMBER: US/09/854,845
CURRENT FILING DATE: 2001-05-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/205,274 PRIOR FILING DATE: 2000-05-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  531 WGSWSKCSSNCGGGMQSRRRACENGNSCLGCGVEFKTCNPEGCPEVRRNTPWTP 584
                                                                                                                                                                                                                                      531 WGSWSKCSSNCGGGMQSRRRACENGNSCLGCGVEFKTCNPEGCPEVRRNTPWTP 584
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nes 15; Conserva
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Wang, Xiaoming
Scoville, John
Turner, C. Alexander Jr.
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27.8%;
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Pred. No. 34;
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Pred. No. 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: homo sapiens US-09-854-845-2
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US-09-854-845-2
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US-09-854-845-8
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APPLICANT: Walke, D
APPLICANT: Wang, X
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Best Local Similarity
Matches 15; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                  GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09854845 Patent No. US20020098491A1
                                                                                                                                                                                                                       Sequence 8, Application US/09854845 Patent No. US20020098491A1
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Best Local S
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             APPLICANT: Walke, D. Wade
APPLICANT: Wang, Xiaoming
APPLICANT: Wang, Xiaoming
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020098491Alel Human Semaphorin Homologs and Polynucleo
FILE REFERENCE: LEX-0177-USA
CURRENT APPLICATION NUMBER: US/09/854,845
CURRENT FILING DATE: 2001-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/854,845
CURRENT FILLING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 60/205,274
PRIOR FILING DATE: 2000-05-18
PRIOR PELICATION NUMBER: US 60/208,893
PRIOR PELICATION NUMBER: US 60/208,893
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020098491A1el Human Semaphorin Homologs and Polynucleo
FILE REFERENCE: LEX-0177-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 10
TYPE: PRT
PRIOR APPLICATION NUMBER: US 60/205,274
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                                                                                                                                                                                                                                                                                                                                                                626 WGSWSKCSSNCGGGMQSRRRACENGNSCLGCGVEFKTCNPEGCPEVRRNTPWTP 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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27.8%;
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Pred. No. 37;
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Pred. No. 38;
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RESULT 8
US-09-854-845-12
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; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-8
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Best Local Similarity
Matches 15; Conserv
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Patent No. US20020098491A1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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Patent No. US20020098491A1
GENERAL INFORMATION:
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                APPLICANT: Walke, D. Wade
APPLICANT: Wang, Xiaoming
APPLICANT: Wang, Xiaoming
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: NO. US20020098491A1el Human Semaphorin Homologs and Polynucleotid
FILE REFERENCE: LEX-0177-USA
CURRENT FALING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 60/205,274
PRIOR APPLICATION NUMBER: US 60/205,274
PRIOR APPLICATION NUMBER: US 60/208,893
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 50
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APPLICANT: Wang, xiaoming
APPLICANT: Wang, xiaoming
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, No. US20020098491A1el Human Semaphorin Homologs and Polynucleotid
FILE REFERENCE: LEX-0177-USA
CURRENT APPLICATION NUMBER: US/09/854,845
CURRENT FILING DATE: 2001-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/205,274
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: US 60/208,893
PRIOR FILING DATE: 2000-06-02
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TYPE: PRT
ORGANISM: homo sapiens
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NUMBER OF SEQ ID NOS: 50
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PRIOR APPLICATION NUMBER: US 60/208,893
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FastSEQ for Windows Version 4.0
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27.8%;
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Pred. No. 40;
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Pred. No. 39;
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; LENGTH: 1151
; TYPE: PRT
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Best Local S
Matches 15
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LENGTH: 1136
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APPLICANT: Wang, Xiaoming
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: No. US20020098491A1e1 Human Semaphorin Homologs and Polynucleo
FILE REFERENCE: LEX-0177-USA
CURRENT APPLICATION NUMBER: US/09/854,845
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 60/205,274
PRIOR APPLICATION NUMBER: US 60/208,893
PRIOR APPLICATION NUMBER: US 60/208,893
PRIOR FILING DATE: 2000-06-02
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APPLICANT:
APPLICANT:
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             APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR US
                                                                                                                                                                                                                                                                                                                              APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
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FILE REFERENCE:
                                                                                                            APPLICANT:
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                                                                    Clapper, Jonathan D.
Skeiky, Yasir A. W.
Fanger, Gary R.
Vedvick Thomas S.
                                                                                                                                         King, Gordon E.
Wang, Aijun
                                                                                                                                                                        Jiang, Yuqıu
Smith, Carole L.
                                                                                                                                                                                                                  Stolk, John A. Wang, Tongtong
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                                                                                                                                                                                                                                                                         Secrist, Heather
Benson, Darin R.
                                                                                                                                                                                                                                                                                                           Lodes, Michael
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210121.471C14
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27.8%;
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Pred. No. 42;
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Pred. No. 4
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US-09-922-217-1116
; Sequence 1116, Application US/09922217
; Patent No. US20020076414A1
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LENGTH: 5405
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Best Local
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Best Local Similarity 41.4
Matches 12; Conservative
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                                                                                                                                                                                                       Publication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Clapper, Jonathan D.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ. ID NOS: 1124
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                     APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
CURRENT APPLICATION NUMBER: US/10/001,857
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                       5014 AWRVPGSSKGCG----EGCGP---QGCP 5034
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Smith, Carole Lynn
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Benson, Darin R.
Beagher, Madeleine Joy
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Pred. No. 2.5e+02;
""" matches 7;
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Pred. No. 2.5e+02;
2; Mismatches 7
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; TYPE: PRT; ORGANISM: Homo sapien US-10-001-857-187
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US-09-764-864-1174
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NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.1
SEQ ID NO 187
LENGTH: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A
APPLICANT: Fernandes, Elma
                                                                                                                                         Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1174
LENGTH: 282
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                       Sequence 1174, Application US/09764864 Patent No. US20020132753A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
LENGTH: 1588
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Best Local Similarity
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PRIOR FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/000,512
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/619,252
PRIOR FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Fernandes, Elma
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 15966-556
                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
LOCATION: (41)
OTHER INFORMATION: Xaa
NAME/KEY: SITE
LOCATION: (65)
                                                                                                  TYPE: PRT
ORGANISM: Homo
                                                                       NAME/KEY: SITE
                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               971 EWSNWSRCSKSCGSGVKVRSKWLREK-----PYNG 1000
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45.8%;
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37.1%;
                                    equals any of the naturally occurring L-amino acids
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Pred. No. 5;
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Sequence 800, Application US/09764853

Patent No. US20020090672A1

GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P3706

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 939

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 800
LENGTH: 800

TYPE: PAT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (197)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (201)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (887)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (887)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (887)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (887)
Search completed: January 15, 2003, 08:23:04 Job time: 10.0913 secs
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US-09-764-853-800
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                                                                                                                                                                                                                           Query Match 21.5%; Score 53.5; DB 10; Length 800; Best Local Similarity 41.7%; Pred. No. 50; Matches 15; Conservative 0; Mismatches 16; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 21.7%;
Best Local Similarity 31.4%;
Matches 16; Conservative
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                                                                                                            74 WASWSACSVSCGGGARQRTRGC----SDPVPQYGGR 105
                                                                                                                                                     2 WYSWKRSSKSTGLGDTATREGCGPSQSDGCP-YNGR 36
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Title: Perfect score: Sequence:

US-09-079-819-50
249
1 EWYSMKRSSKSTGLGDTATR......PSQSDGCPYNGRLTTVKPRK 44

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	89	7	თ	IJ	4	w	N	_	No.	Result
·	53.5	Ψ	ω.	ω.	ω.	54	54	54	Δ	54.5	4		5	56		56	57.5	57.5	58.5	58.5	58.5	59	59	64.5	65	65	68	68	Score	
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1376	566	530	331	263	263	1234	438	225	1584	424	412	189	488	1444	301	110	1172	509	2533	2533	1003	1360	394	1572	1522	984	799	417	Length	
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S63986	HMIVAT	S33673	S45584	в37881	S13614	S52099	S70602	н69677	T00026	A54533	OZZQAF	B29795	S67744	T18856	H70644	D72701	A42587	AD0649	T28674	T28675	T13951	T33922	S36512	T00027	T00028	T00326	JH0797	A49129	Ħ	
collagen alpha 5 c	hemagglutinin prec	probable protein k	transcription acti	pollen allergen Lo	major allergen Lol		cellulose 1,4-beta	involved in polyke	_	circumsporozoite p	circumsporozoite p	oite	hypothetical prote			hypothetical prote		probable secreted	alpha-51D-immobili	alpha-51D immobili		۳	E2 protein - human		brain-specific ang	hypothetical prote	castor protein - f	roblast	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	
51	51.5	51.5	51.5	51.5	51.5	52	52	52	53	53	53	53	53	53	53.5	
20.5	20.7	20.7	20.7	20.7	20.7	20.9	20.9	20.9	21.3	21.3	21.3	21.3	21.3	21.3	21.5	
292	951	788	434	388	121	1221	435	177	1327	569	558	226	215	184	1433	
N	N	N	N	N	ш	N	N	N	N	N	N	N	N	N	N	
T14627	T00260	T25061	A39181	A39756	A37331	A44978	JC4590	T19610	T09402	T19483	T17324	T43814	S34163	T46433	A46053	
hypothetical prote	hypothetical prote	hypothetical prote	salicylate 1-monoo	circumsporozoite p	secretory protein	DNA topoisomerase	salicylate 1-monoo	hypothetical prote	immunoglobulin-lik	hypothetical prote	hypothetical prote	conserved hypothet	homeotic protein H	hypothetical prote	bullous pemphigoid	

ALIGNMENTS

RESULT 2 JH0797 castor protein - fruit fly (Drosophila sp.) C.Species: Drosophila sp. C.; Species: Drosophila sp. C.; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2000 C.; Accession: JH0797 R.; Mellerick, D.M.; Kassis, J.A.; Zhang, S.D.; Odenwald, W.F. Neuron 9, 789-803, 1992 A; Mittle: Castor encodes a novel zinc finger protein required for the development of a A; Mittle: Castor encodes a novel zinc finger protein required for the development of A; Mittle: Castor encodes a novel zinc finger protein required for the development of a A; Mccession: JH0797 A; Mclecule type: DNA A; Reference number: JH0797, MUID:93040222; PMID:1418995 A; Cross-references: GB:L04487 C; Genetics: A; Gene: FlyBase:cas A; Cross-references: FlyBase:FBgn0004878 A; Introns: 284/3; 515/3; 660/3 C; Keywords: metal binding; zinc finger F; 236-242/Region: acidic F; 333-421/Region: zinc finger F: 422-448/Region: zinc finger F: 422-448/Region: zinc finger	A; Molecule type: nucleic acid A; Residues: 1-417 <cui> A; Experimental source: embryo A; Experimental source: embryo C; Genetics: A; Gene: FlyBase:cas A; Cross-references: FlyBase:FBgn0004878 Query Match Best Local Similarity 26.3%; Pred. No. 1.1; Matches 10; Conservative 10; Mismatches 18; Indels 0; Gaps 0; Matches 10; Conservative 10; Mismatches 18; Indels 0; Gaps 0; Qy 1 EWYSWKRSSKSTGLGDTATREGCGPSQSDGCPYNGRLT 38 II: :: :: :: :: : Db 155 KWHKKRKESLKLGFARFSSSDDCAPAYGEGCAYNWKQT 192</cui>	RESULT 1 A49129 A49121 A49121 A49121 A49122 A40123 A49122 A49123 A49123 A49123 A49123 A49123 A49123 A49123 A5454545 A5554545 A5554545 A5554545 A5554545 A6555565 A66555665 A66555665 A66555665 A6655665 A6655665 A6655665 A66566565 A66566656
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T00028
T00028

Drain-specific anglogenesis inhibitor 3 - human
N;Alternate names: BAI3 protein
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-J
C;Accession: T00028
C;Accession: T00028
R;Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino,
C;Accession: Cell Genet. 79, 103-108, 1997
                                                                                                                                    C;Superfamily: Lilumbospondin F;344-398/Domain: thrombospondin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani DNA Res. 5, 31-39, 1998
A;Title: Prediction of the coding sequences of unidentified A;Reference number: Z14086; MUID:98290545; PMID:9628581
A;Accession: T00326
                                                                                                                                                                         A;Cross-references: GDB:9838090; OMIM:602684
A;Map position: 6q12-6q12
C;Superfamily: thrombospondin type 1 repeat homology
                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-1522 <SHI>
A;Cross-references: EMBL:AB005299; NID:g3021700; PIDN:BAA25363.1; PID:g3021701
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                        Cytogenet. Cell Genet. 79, 103-108, 1997
A;Title: Cloning and characterization of Ba
A;Reference number: Z14066; MUID:98194217;
A;Accession: T00028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AB011122; NID:g3043623; PIDN:BAA25476.1; PID:g3043624 A;Experimental source: brain C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-984 <NAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein KIAA0550 - human C;Speckes: Homo sapiens (man) C;Deckes: Homo sapiens (man) C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000 C;Accession: T00326
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F;542-600/Region:
                                                                                                                                                                                                                                    A; Gene: GDB:BAI3
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Best Local :
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EWSPWSLCSFTCGRGQRTRTRSCTPPQYGGRPCEGPETHHKP
                                      EWYSWKRSSKSTGLGDTATREGCGPSQSDGCPYNGRLTTVKP 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EWSPWSLCSFTCGRGQRTRTRSCTPPQYGGRPCEGPETHHKP 391
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zinc
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                                                                                                                                                        type 1 repeat homology <THR3>
                                                                                             Score 65;
Pred. No.
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Pred. No. 5
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5.6;
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8.3;
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                                                                                           R;Courtney, L.; Langston, Y.; Drone, K.; Mead, K. submitted to the EMBL Data Library, February 1999 A;Description: The sequence of C. elegans cosmid
                                                                                                                                                                       hypothetical protein Y8A9A.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct_1999  #sequence_revision 29-Oct-1999  #text_change 29-Oct-1999
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                                                      A; Reference number: A; Accession: T33922
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                A; Molecule type:
                                    A; Status: preliminary; translated
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T33922

DNA

from GB/EMBL/DDBJ

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A;Molecule type: mRNA
A;Residues: 1-1572 <SHI>
A;Cross-references: EMBL:AB005298; NID:g3021698; PIDN:BAA25362.1; PID:g3021699
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Cytogenet. Cell Genet. 79, 103-108, 1997
A;Title: Cloning and characterization of BAI2 and BAI3, A;Reference number: Z14066; MUID:98194217; PMID:9533023 A;Accession: T00027
                                                         Query Match
Best Local Similarity
"~+~hes 12; Conserva
                                                                                                                                               A;Cross-references: EMBL:X74475; NID:g396981; PIDN:CAA52552.1; PID:g396985 C;Superfamily: papillomavirus E2 protein C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                             C;Accession: S36512
R;Delius, H.; HOfmann, B
submitted to the EMBL Data Library, August
A;Description: Primer-directed sequencing of
                                                                                                                                                                                                                                                                                                                                      E2 protein - human papillomavirus type : C;Species: human papillomavirus type 32 C;Date: 20-Feb-195 #sequence_revision : C;Accession: S36512
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                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-394 <DEL>
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A;Cross-references: GDB:9838089; OMIM:602683
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Best Local (
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                         17 TATREGCGPSQSDGCPYNGRLTTVKPRK 44
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les 15; Conserv
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TITRSNCDPDGTDGILYKDPTPTTPPRK
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                                                                                        Score 59;
Pred. No.
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Pred. No. 9
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8, 1997
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of human
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13;
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C; Accession: T13951
R; Seki, M; Katada, T; Enomoto, T.
Biochim. Biophys. Acta 1396, 127-131, 1998
A; Title: Isolation of a cDNA encoding mouse DNA topoisomerase
A; Reference number: Z17829; MUID:98201702; PMID:9540825
A; Accession: T13951
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                                                       õ
                                                                                                                                                                       A; Genetic code: SGC5
A; Introns: 280/3; 538/2;
C; Superfamily: G surface
                                                                                                                                                                                                                                                                                                                                              R;Schwegmann, K.J.
submilted to the EMBL Data Library,
A;Reference number: Z20506
A;Accession: T28675
                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-51D immobilization antigen - Paramecium tetraurelia C;Species: Paramecium tetraurelia C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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C; Keywords:
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                                                                                                                                                                                                                                    A;Gene:
                                                                                                                                                                                                                                                 C; Genetics
                                                                                                                                                                                                                                                                     A; Cross-references:
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A; Residues: 1-2533 <SCH>
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                       KTCKLAENQTDGSCG-SFLDGCVYNGNAGCVDPK 732
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                                                                                                                                                                                                                                                                                                                          preliminary; translated
                                                         KSTGLGDTATREGCGPSQSDGCPYNGRLTTVKPR 43
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protein
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                                                                                            Score 58.5; Depred. No. 82; Mismatches
                                                                                                                                                                                                                                                                     PIDN: CAA65264.1
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, S.; Moule, !
                                 C:Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
C;Accession: A42587; A39851
R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.J. Biol. Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Accession: A42587
                                                                                                                                                                                                            RESULT 12
A42587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Schmidt, H.J.
submitted to the EMBL Data
submitted to umber: 220505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; PMID:11677608
A;Accession: AD0649
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C; Date: 15-Oct-1999 #sequence_revision
                                                                                                                                                                                      thrombospondin 2 precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-509 < P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: AD0649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable secreted protein STY1292 [imported] - Salmonella enterica subsp.
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                 A; Status: preliminary; not compared
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X85135; NID:g728634; PID:g728635; PIDN:CAA59447.1
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A; Molecule type: nucleic
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Best Local S
Matches 17
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                                                                                                                                                                                                                                                                                                                      1 EWYSWKRSSKSTGLGDTATREGCGPS--QSDGCPYNGRLTTVKPRK
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Pred. No. 25;
6; Mismatches
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Pred. No. 82;
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                                                                                                              Seldin, M.F.; Dixit, V.M
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                                                                          and expression during
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P.; Dixit, V.M. PID:g567241

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A;Cross-references: GB:M64866; NID:g201994; PIDN:AAA40432.1; PJC;Superfamily: thrombospondin 1; EGF homology; thrombospondin t C;Superfamily: thrombospondin 1; EGF homology; thrombospondin t C;Superfamily: von Willebrand factor type C repeat homology F;380-431/Domain: thrombospondin type 1 repeat homology <THR1>F;480-492/Domain: thrombospondin type 1 repeat homology <THR2>F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>F;453-588/Domain: EGF homology <EGF1>F;652-691/Domain: EGF1
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A;Note: sequence extracted from NCBI backbone (NCBIP:81502)
R;Bornstein, P; O'Rourke, K; Wikstrom, K; Wolf, F.W.; Katz, R.; Li, P
J. Biol. Chem. 266, 12821-12824, 1991
A;Title: A second, expressed thrombospondin gene (Thbs2) exists in the m
A;Reference number: A39851; MUID:91302287; PMID:1712771
A;Accession: A39851
A;Status: preliminary
A;Residues: 1-873 <BOR>
                     hypothetical protein Rv0725c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: H70644
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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awa, H.; Takamiya, M.; Masuda,
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequer
A;Reference number: A72450; MU
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H70644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: DDBJ:AP000060;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1027
C;Superfamily: Aeropyrum pernix hyp
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A;Molecule type: DNA
A;Residues: 1-110 <KAW>
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Rajandream,
Nature 393,
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M.A.; RO
537-544,
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   Rogers,
44, 1998
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50; MUID:99310339; PMID:10382966
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, S.; Funahashi, T.; Tanaka,
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Pred. No. 54;
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Search completed: January Job time: 6.26484 secs

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submitted to the EMBL Data Library,
A; Reference number: Z19031
A; Accession: T18856
A; Status: preliminary; translated fi
A; Molecule type: DNA
A; Residues: 1-1444 <WIL>
A; Cross-references: EMBL: Z50004; PII
A; Cross-references: EMBL: Z50004; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70644
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-301 <COL>
A;Cross-references: GB:Z84395; GB:AL123456; NID:g3261698; PIDN:CAB06449.1; PID:g1
                                                                                                                                                                                                                                                                                                     R;McMurray, A.
submitted to the EMBL Data
submitted to number: Z19917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angiogenesis inhibitor homolog - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T18856; T24653
R;McMurray, A.
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T18856
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                                                                                                                A; Gene: CESP: CO2:
A; Map position:
A; Introns: 25/3;
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ce: clone T07C5
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NHG2_PSEPU
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CSP_PLARE
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GUX3_AGABI
MPL1_LOLPR
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TSP2_MOUSE
SM5B_MOUSE
 MKR2_SERQU
PROP_MOUSE
Y194_HUMAN
CSP_PLAFO
DPYS_RAT
YVD3_CAEEL
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XP2_XENLA
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sagaricus bi

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1 homo sapien
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RESULT 1

BAI3_HIMAN
ID BAI3_HI
AC 060242
DT 16-OCT
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DE BAI3 0
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OC EURAPY
OC Mammal
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RP SEQUEN
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Genew; HGNC:945; BAI3
MIM; 602684; -.
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MEDLINE=98194217; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Brain;
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4.0	4.9	49	45	49	49	49	4.0	49.5	49.5	49.5	49.5
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461	392	359	339	303	292	281	129	1628	799	660	566
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VE2_HPV09	NADD_UREPA	GUN1_STRSQ	HXD9_MOUSE	BNK_DROME	NIFH_KLEPN	YH71_AERPE	VAL2_THOV	NAGH_CLOPE	ITBN_DROME	VE1_HPV29	HEMA_IATKI
	Q9pq21 ureaplasma	P13933 streptomyce					Q06658 tomato mott				P11135 influenza a

ALIGNMENTS

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A MEDLINE-9829045; PubMed-9628581;

A Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,

Nomura N., Ohara O.;

Prediction of the coding sequences of unidentified human genes. IX.

The complete sequences of 100 new cDNA clones from brain which can

recode for large proteins in vitro.";

LDNA Res. 5:31-39(1998).

LDNA Res. 5:31-39(1998).

C -:- FUNCTION. MIGHT BE INVOLVED IN ANGIOGENESIS INHIBITION AND

SUPPRESSION OF GLIOBLASTOMA.

C -:- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A

C SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.

--- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN BRAIN. ALSO DETECTED IN
                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        LINES.
-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
-!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
-!- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
-!- SIMILARITY: CONTAINS 1 GPS DOMAIN.
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060242; 060297;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Brain-specific angiogenesis inhibitor 3 precursor.
BAI3 OR KIAA0550.
EMBL; AB005299; BAA25363.1; -. EMBL; AB011122; BAA25476.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shiratsuchi T., Nishimori H., Ichise H., Nakamura Y., "Cloning and characterization of BAI2 and BAI3, novel to brain-specific angiogenesis inhibitor 1 (BAII)."; Cytogenet. Cell Genet. 79:103-108(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEART. REDUCED EXPRESSION IS OBSERVED IN SOME GLIOBLASTOMA CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=9533023;
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                                                                                                                                           noved. Usage by and for (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes homologous
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Pfam; PF00090; tsp_1; 4.

Pfam; PF01825; GPS; 1.

Pfam; PF01825; GPS; 1.

SMART; SM00303; GPS; 1.

SMART; SM00303; GPS; 1.

SMART; SM00209; TSP1; 4.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01221; GPS; 1.

PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FAPROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.

PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.

PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.

PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.

PROSITE; PS50092; TSP1; 4.

G-PROTEIN COUPLED TSP1; 4.
                                                                                                                                                                                                                                                                                                     CARBOHYD
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350
                                            1 EWYSWKRSSKSTGLGDTATREGCGPSQSDGCPYNGRLTTVKP 42
  EWSPWSLCSFTCGRGQRTRTRSCTPPQYGGRPCEGPETHHKP 391
                                                                                                Similarity
15; Conserv
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IPR000832;
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; GPCR_secretin.
; PKD_cys_rich.
; TSP1.
                                                                                                                       26.1%;
35.7%;
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CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).
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OCCUPANCE OF COLORD.

N-LINKED (GLCNAC. . .) (POTEN
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CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).
                                                                                             Score 65; DB Pred. No. 1.8; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Glycoprotein; Signal,
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TSP TYPE-1 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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                                                                                                                    1.8;
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                                                                                                                                              Length 1522
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BAIZ_HUMAN
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AC CO0241
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SMART; SM00209; TSP1; 4.

SMART; SM00209; TSP1; 4.

PROSITE; PS50221; GPS; 1.

PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; F7

PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; F7

PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.

PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.

PROSITE; PS50262; TSP1; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000203; PKI
InterPro; IPR000884; TS:
InterPro; IPR001879; ho
Pfam; PF00002; 7tm_2; 1
Pfam; PF000000; tsp_1; 4
Pfam; PF00090; tsp_1; 4
Pfam; PF01825; GPS; 1.
Pfam; PF02793; HRM; 1
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060241;
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DOMAIN
                                                                                                                                                                                                                                                                                               Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shiratsuchi T., Nishimori H., Ichise H., Nakamura Y., Tokin "Cloning and characterization of BAI2 and BAI3, novel genet to brain-specific angiogenesis inhibitor 1 (BAI1).", Cytogenet. Cell Genet. 79:103-108(1997).

-i- FUNCTION: MIGHT BE INVOLVED IN ANGIOGENESIS INHIBITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: Integral membrane protein.
-I- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN BRAIN. ALSO DETECTED HEART, THYMUS, SKELETAL MUSCLE, AND DIFFERENT CELL LINES.
-I- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS
-I- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
-I- SIMILARITY: CONTAINS 1 GPS DOMAIN.
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Brain-specific angiogenesis inhibitor 2 precursor.
                                                                                                                                                                                                                                                                                                                                          G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Fetal brain; MEDLINE-98194217; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Fetal
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; PKD_cys_rich.
; TSP1.
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                         4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

5 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                          Transmembrane; Glycoprotein; Signal;
                                                                                                                          EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL)
                                                                                                 CYTOPLASMIC
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1 (POTENTIAL)
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RESULT 3

VE2_HPV32

ID VE2_HPV32

AC P36791;
DT 01-JUN-199,
DT 15-JUL-199,
DT 15-JUL-199,
DT 02-JUN-199,
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Best Local
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SEQUENCE
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DOMAIN
                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29,
01-JUN-1994 (Rel. 29,
15-JUL-1998 (Rel. 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses,
    EMBL; X74475; CAA52552.1;
                                                                                                                                                                                                                                                                                                       Delius H., Hofmann B.;
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10612;
                                                                                                                                                                                                                                                                                                                                                                            Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                 Regulatory protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EWYSWKRSSKSTGLGDTATREGCGPSQSDG------CPYNGR 36
                                                                                                                                        SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                     REPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                      papillomavirus
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                                                                                                                                                                                                                                                                                                                      PubMed-8205838;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                        32
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Pred. No. 2.2;
3; Mismatches
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EXTRACELLULAR
7 (POTENTIAL).
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POLY-ASN.
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POLY-PRO.
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                        Pfam; PF00098; zf-CCHC; 1.
Pfam; PF01131; Topoisom_bac; 1.
Pfam; PF011396; zf-C4_Topoisom; 1
Pfam; PF01751; Toprim; 1.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00417; PRTPISMAASEI.
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PRINTS; PRINTS; SMART; S

TOP1Ac;

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RESULT 4
TP3A_MOUSE
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InterPro; IPR00380; DNAtopI_NAP_bind.
InterPro; IPR003601; DNAtopI_NAP_bind.
InterPro; IPR003602; DNAtopI_NAP_bind.
InterPro; IPR003800; Prok_tpisomrasconterpro; IPR001878; Znf contentPro; IPR00188; Znf contentPro; IP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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Interpro; IPR000427; E2_C.
Interpro; IPR001866; E2_N.
Pfam; PF00508; E2_N; 1.
Pfam; PF00511; E2_C; 1.
ProDom; PD000678; E2_N; 1.
ProDom; PD000678; E2_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seki T., Seki M., Katada T., Enomoto T.;
"Isolation of a cDNA encoding mouse DNA topoisomerase III which
highly expressed at the mRNA level in the testis.";
Biochim. Biophys. Acta 1396:127-131(1998).
-!- FUNCTION: REDUCES THE NUMBER OF SUPERCOILS IN A HIGHLY NEGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Testis;
MEDLINE-98201702; PubMed-9540
                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                          the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA, followed by passage and rejoining. TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III:
                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
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P; P17383;
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39, Last annotation update)
III alpha (EC 5.99.1.2).
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42.9%;
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replication; Repressor; Nuclear protein
8 MW; 113C46119C2265E7 CRC64;
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Sciurognathi; Muridae;
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RESULT 5
TSP2_MOUSE
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01-JUN-1994 (Ret. 2
16-OCT-2001 (Ret. 4
                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/www.isb-sentitles.com/server/w
                                                                                                                                                                                                                                                                                                                                                                                                                                    genome.";
J. Biol. Chem. 266:12821-12824(1991).
-I- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND
-I- TO CAMBEN THERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSP2_MOUSE
Q03350;
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ACT_SITE
DOMAIN
DOMAIN
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SMART; SN
PROSITE;
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Laherty C.D., O'Rourke K., Wolf F.W.,
Dixit V.M.;
                                                                                                                                        entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: HOMOTRIMER: DISULFIDE-LINKED.
-!- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
-!- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
-!- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
-!- SIMILARITY: CONTAINS 7 TSP TYPE-3 DOMAINS.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
                                                                              EMBL; L07803; AAA53064.1; EMBL; M64866; AAA40432.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91302287; PubMed-1712771;
Bornstein P., O'Rourke K., Wikstrom K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of mouse thrombospondin during cell growth and development.";
J. Blol. Chem. 267:3274-3281(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombospondin
THBS2 OR TSP2.
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                                                                                                                                                                                                                                                                                                                                                                                                                            CELL-TO-MATRIX INTERACTIONS. CAN BIND LAMININ AND TYPE V COLLAGEN.
                                    A42587; A42587.
A39851; A39851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WYSWKRSSKSTGLGDTATREGCGPSQSDGCP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM00493;
SM00343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Topolsomerase; 1
362 362
658 685
814 925
814 841
898 925
1003 AA; 11235
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: 1EDM.
38; Thbs2
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ZnF_C2HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 29, Created)
. 29, Last sequence update)
. 40, Last annotation update)
precursor.
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112358 MW;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254C738E746EE495 CRC64;
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                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wolf F.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
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Best Local S
Matches 17
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Pfam; PF00093; vwc; 1.
Pfam; PF02210; TspN; 1.
Pfam; PF02412; tsp_3; 9.
SMART; SM00181; EGF; 3.
SMART; SM00209; TSPN; 1.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 1.
                                                                                                                               DISULFID
DISULFID
CARBOHYD
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DISULFID
                                                                                      CARBOHYD
CARBOHYD
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DOMAIN
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CHAIN
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PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
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InterPro;
                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; EGF-like doma
                                                                                                                         CARBOHYD
                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                           DOMAIN
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                                                                                                     CARBOHYD
                                                                                                           CARBOHYD
                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
502
                          443
             42
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             ש
                                  WYSWKRSSKSTGLGDTATR---
                          WSPWSSCSVTCGVGN-VTRIRLCNSPVPQMGGKNCKGSGRETKPCQRDPCPIDGRWSPWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00008;
502
             42
                                                                                                                                                                                                                                                                                                                                                               PS00022; EGF_1;
PS01186; EGF_2;
PS50092; TSP1; 3;
PS01208; VWFC; 1
                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                domain; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001007;
IPR003367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000561;
IPR001881;
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                                                                                 Cell adhesion;
                                                                                 AA;
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3.
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TSPN.
VWF_C.
tsp_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-like.
EGF_Ca.
                                                                                 129911 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laminin_G
                                                            .98;
                                                                              BY SIMILARITY.
CLINKED (GLCNAC...)
LINKED (GLCNAC...)
LINKED (GLCNAC...)
LINKED (GLCNAC...)
VARED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                    FALSE_NEG
                                                     Score 57.5; I
Pred. No. 13;
6; Mismatches
                                                                                                                                                                                                                             TSP TYPE-1 2

TSP TYPE-1 3

EGF-LIKE 2,

EGF-LIKE 3,

TSP TYPE-3 3

TSP TYPE-3 3

TSP TYPE-3 3

TSP TYPE-3 5

TSP TYPE-3 5

TSP TYPE-3 5

TSP TYPE-3 7

TSP TYPE-3 7
                                                                                                                                                                                                                                                                                                                                                        Calcium-binding; Heparin-binding; Repeat;
                                                                                                                                                                                                         CELL ATTACHMENT SITE (POTENTIAL).
INTERCHAIN (PROBABLE).
                                                                                                                                                                                                                        C-TERMINAL
                                                                                                                                                                                                                                                                                                                              HEPARIN-BINDING
                                                                                                                                                                                                                                                                                                                                    THROMBOSPONDIN
                                                           9 57.5; NO. 13;
                                       ---EGCG----PSQSDGCPYNGRLTTVK 41
                                                                                                                                                                                                                                                                                    CALCIUM-BINDING
                                                                   DB
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                                                     17;
                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                 Length
                                                                                 CRC64;
                                                     Indels
                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                    Gaps
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RESULT 6
SMSB_MOUSE
ID S_MOUSE
ID S_MOUSE
ID 30-MAY
DT 30-MAY
OC MEMBAI
RR MEDLIN
RR MEDLIN
RR MEDLIN
CC -!- SI
COMAII
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FT CARBO
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                                                                                                                                                                                                                                                                                                                               Pfam; PF00090; tsp_1; 5.
Pfam; PF01403; Sema; 1.
Pfam; PF01437; PSI; 1.
SMART; SM00423; PSI; 1.
SMART; SM00209; TSP1; 4.
                 CARBOHYD
CARBOHYD
                                                                                                                DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mech. Dev. 57:33-45(1996).

I FUNCTION: MAY ACT AS POSITIVE AXONAL GUIDANCE CUES.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: IN ADULT, ONLY DETECTED IN BRAIN.

BYELOPMENTAL STAGE: DIFFERENTIALLY EXPRESSED IN EMBRYONIC ADULT TISSUES. ITS ABUNDANCE DECREASES FROM ELO TO BITH.

SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.

SIMILARITY: CONTAINS 1 SEMA DOMAIN.
                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalla; Eutherla; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Semaphorin 5B precursor (Semaphorin G) (Sema (SEMASB OR SEMAG OR SEMG)
                                             CARBOHYD
                                                          CARBOHYD
                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                      PROSITE; PS50092; TSP1; 6.
Signal; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams R.H., Betz H., Pueschel A.W.;
"A novel class of murine semaphorins with homology to thrombospondin is differentially expressed during early embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM5B_MOUSE
                                                                         CARBOHYD
                                                                                       CARBOHYD
                                                                                                     DOMAIN
                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96414430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                        Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            x97818;
                                                                                                                                                                                                                                                                                                                                                                                                     IPR003659; Plexin-like.
IPR002165; Plexin_repeat.
IPR001627; Sema.
IPR000884; TSP1.
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9799
1000
2366
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6664
721
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852
969
959
157
178
333
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7193
663
663
776
851
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178
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Rodentia;
                                                                                                                                                                                                                                                                                         Glycoprotein
 N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                 SEMA.
TSP I
                                                                                     N-LINKED
                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                             SEMAPHORIN 5B.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                            POTENTIAL.
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Sciurognathi;
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                                                                                                                                                                                                                                                                                                  Multigene family; Neurogenesis;
                                                                                                                             TYPE-1
TYPE-1
TYPE-1
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(GLCNAC.
(GLCNAC.
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(POTENTIAL).
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Cr. 01-OCT-1996 (Rel. 34, La 16-OCT-2001 (Rel. 40, La SCO-spondin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSPO_BOVIN
P98167;
01-OCT-1996
01-OCT-1996
16-OCT-2001
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CARBOHYD
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TISSUE-Ependymocyte;
MEDLINE-96338614; PubMed-8743952;
MEDLINE-96338614; PubMed-8743952;
Gobron S., Monnerie H., Meiniel R., Creveaux I., Lehmann W
Lamalle D., Dastugue B., Meiniel A.;
                               Pfam;
Pfam;
Pfam;
Pfam;
                                                                                                                                                 EMBL;
HSSP;
                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                           - I- DEVELOPMENTAL STAGE: EMBRYO.
- I- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
- I- SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.
- I- SIMILARITY: CONTAINS AT LEAST 2 EGF-LIKE DOMAINS.
- I- SIMILARITY: CONTAINS AT LEAST 1 F5/8 TYPE C DOMAIN.
- I- SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOVIN
                                                                              Pfam;
                                                                                                                                                                                   or send
                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 WYSWKRSSKSTGLGDTATREGCGPSQSDGCP-YNGRLTTVKPRK
                               PF00090;
PF00093;
PF00754;
PF01826;
                                                                                                                                                 X93922; CAA63815.1; -. P01130; lAJJ.
                                                                               PF00057;
                                                                                                                                                                                   s requires a license agreement (S
an email to license@isb·sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                   IPR000884;
                                                                                                              IPR002919;
                                                                                                                            IPR002172;
                                                                                                                                     IPR000421;
                                                                                         IPR001007; VWF_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                    ; F5_F8_type_C;
; TIL; 1.
1; FA58C; 1.
                                                                             ldl_recept_a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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A
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539
547
547
602
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944
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                                                                                                   TIL_Cysrich.
TSP1.
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Pred. No. 16;
7; Mismatches
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| CSP_DLAFL STAN

| P05691;

| 01-NOV-1988 (Rel. 0

| 01-NOV-1988 (Rel. 0

| 01-FEB-1994 (Rel. 2
              "Sequence variation of Plasmodium tatter-circumsporozoite protein of Plasmodium tatter-vaccine development.";

J. Biol. Chem. 262:11935-11939(1987).

-I- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS SURFACE ANTIGEN ON THE SPOROZOITE (THE INF
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01-NOV-1988 (Rel. 09, Last sequence update
01-FEB-1994 (Rel. 28, Last annotation update
Circumsporozoite protein (CS) (Fragment).
Plasmodium falciparum (isolate le5).
Plasmodium falciparum (isolate le5).
Eukaryota; Alveolata; Apicomplexa; Haemosi
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MEDLINE-87308186; PubMed-2442154;
La Cruz V.F., Lal A.A., McCutchan T.F.;
"Sequence variation in putative functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein;
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TE; PS01285; FA58C_1;
TE; PS01286; FA58C_2;
TE; PS01209; LDLRA_1;
TE; PS0068; LDLRA_2;
TE; PS50092; TSP1; 4
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TSP TYPE-1 3.
TSP TYPE-1 3.
TSP TYPE-1 4.
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EGF-LIKE 2.
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F5/8 TYPE C.
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the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                            EMBL; M17802; AAA29538.1; -.
                                                                                                                                                                                                                                                                                   ANCHORING THE PROTEIN TO THE CELL MEMBRANE. '
WYSLKKNSRSLGENDDGNNNNGDNGREGKDEDKRDG
                       WYSWKRSSKSTGLGDTAT-----
                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                               Sporozoite; Repeat.
                                                          21.9%;
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                                              Score 54.5; D
Pred. No. 8.1;
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                       REGCGPSQSDG
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PRT; 412 AA.

""""" (Rel. 01, Created)

"" 16-OCT-2001 (Rel. 01, Last sequence update)

DE Circumsporozoite protein precursor (CS).

"S Plasmodium falciparum.

"Eukaryota; Alveolata; Apicom"

"NCBI_TaxID=5833;

[1]

SEO"""" EMBL; K02194; AAA29524.1; -.
p1R; A03388; OZZQAF.
InterPro; IPR003067; Crcmsprzoite
InterPro; IPR003084; TSP1.
pfam; PF00090; tsp_1; 1. Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Williams J.L., Haynes J.D., Schneider I., F. Sanders G.S., Reddy E.P., Diggs C.L., Miller L.H.; "Structure of the gene encoding the immunodominant surfathe sporozoite of the human malaria parasite Plasmodium Science 225:593-599(1984). or send an email to license@isb-sib.ch). MEDLINE=84250215; PubMed=6204383; FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS SURFACE ANTIGEN ON THE SPOROZOITE (THE INF MALARIA PARASITE THAT IS TRANSMITTED FROM VERTEBRATE HOST).

MISCELLANEOUS: THE C-TERMINAL REGION IS PROMATICELLANEOUS: ANCHORING THE PROTEIN TO THE CELL MEMBRANE. T WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN. SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Enteropean Bioinformatics Institute. There are no restroy non-profit institutions as long as its content this statement CRCMSPRZOITE. THE C-TERMINAL REGION IS PROBABLY USED license Apicomplexa; Haemosporida; Signal. PROBABLE. agreement is not removed. (See IS THE IMMUNODOMINANT INFECTIVE STAGE OF THE ROM THE MOSQUITO TO THE Usage THE J.L., Wirtz der I., Rober Plasmodium surface REPEAT SEQUENCES restrictions Roberts and falciparum. EMBL FOR a collaboration MBL outstation antigen R.A., for ch/announce, ons on its in no way commercial ... g

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PIR; A54533; A54533.

InterPro; IPR003067; Crcmsprzoite.

InterPro; IPR000084; TSP1.

Pfam; PF00090; tsp_1; 1.

PRINTS; PR01303; CRCMSPRZOITE.

SMART; SM00209; TSP1; 1.

Malaria; Sporozoite; Repeat; Signal.

SIGNAL 1 16

PROBABI
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P13814;
01-JAN-1990
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01-JAN-1990 (Rel. 13, Last sequence upda
16-OCT-2001 (Rel. 40, Last annotation upda
Circumsporozoite protein precursor (CS)
Plasmodium falciparum (isolate t4 / Tha
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87315205; PubMed-3306373; Gel Portillo H.A., Nussenzweig R.S., Er "Circumsporozoite gene of a Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Haemosporida; NCBI_TaxID=5846;
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SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                         Biochem. Parasitol. 24:289-294(1987).
FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO TH
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Pred. No. 11;
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SMART; SM00303; GPS; 1.

SMART; SM00008 HOTMR; 1.

SMART; SM00209; TSP1; 5.

PROSITE; PS50021; GPS; 1.

PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FA
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FA
PROSITE; PS50027; G_PROTEIN_RECEP_F2_3; 1.

PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
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16-OCT-2001
16-OCT-2001
15-JUN-2002
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Biochem. Biophys. Res. Commun. 247:597-604(1998).

-i- FUNCTION: LIKELY TO BE A POTENT INHIBITOR OF ANGIOGENESIS IN
BRAIN AND MAY PLAY A SIGNIFICANT ROLE AS A MEDIATOR OF THE P5
SIGNAL IN SUPPRESSION OF GLIOBLASTOMA. MAY FUNCTION IN CELL
ADHESION AND SIGNAL TRANSDUCTION IN THE BRAIN.

-i- SUBUNIT: INTERACTS WITH BAPI.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. LIKELY TO BE
CONCENTRATED AT CELL-CELL ADHESION SITES.

-i- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN BRAIN. REDUCED (
EXPRESSION IS OBSERVED IN SOME GLITORILAGROUM CERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -I- INDUCTION: BY P53.
-I- DOMAIN: THE TSP1 REPEATS INHIBIT IN CORNEA INDUCED BY BFGF.
-I- SIMILARITY: BELONGS TO FAMILY 2 OF G-I- SIMILARITY: CONTAINS 5 TSP TYPE-1 DC-I- SIMILARITY: CONTAINS 1 GPS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB-Fetal brain;
MEDLINE-98054121; PubMed-9393972;
Nishimori H., Shiratsuchi T., Urano T., Kimura Y., Kiyono K.,
Nishimori H., Shiratsuchi T., Urano T., Kimura Y., Tokino T.;
Tatsumi K., Yoshida S., Ono M., Kuwano M., Nakamura Y., Tokino T.;
"A novel brain-specific p53-target gene, BAII, containing
"A novel brain-specific p53-target gene, BAII, containing
thrombospondin type I repeats inhibits experimental angiogenesis.";
Oncogene 15:2145-2150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAII.
Homo sapiens (Human).
Homo sapiens (Human).
""" Metazoa; Chordata;
""" Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH BAP1
MEDLINE=98321173; PubMed=9647739;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB005297; BAA23647.1;
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                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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TISSUES.
                                                                                                                                                                                                                                                                           ; PF00002; 7tm_2; ; PF00090; tsp_1; ; PF01825; GPS; 1. ; PF02793; HRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602682;
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
(Rel. 41, Last annotation update)
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Transmembrane; Glycoprotein; Signal;
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                                                                                                          FALSE_NEG
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Best Local (
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                           STRALE-194368092; PubMed-8083021,
MEDLINE-94368092; PubMed-8083021,
Chow C.-M., Yague E., Raguz S., Wood D.A., Thurston C.F.
The cell gene of Agaricus bisporus codes for a modular
is transcriptionally regulated by the carbon source.";
is transcriptionally regulated by the carbon source.";
                                                                                                                                                                                     AGABI
GUX3_AGABI
P49075;
01-FEB-1996
01-FEB-1996
15-JUL-1999
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01-FEB-1996 (Rel. 33, Last seq
15-JUL-1999 (Rel. 38, Last anno
Exoglucanase 3 precursor (EC 3
(1,4-beta-cellobiohydrolase 3)
SEQUENCE FROM N.A. TISSUE-Mycelium; MEDLINE-96269930;
                                                                                                                             Agaricus bisporus (Commor
Eukaryota; Fungi; Basidio
Agaricales; Agaricaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                        STRAIN-D649
                                                                                                 SEQUENCE FROM N.A.,
                                                                                                                     NCBI_TaxID=5341;
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16; Conserv
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                                                                                                                                                                                                                                                                                                                      Conservative
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el. 38, Last annotation update)
precursor (EC 3.2.1.91) (Exocellobiohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hesion.
                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                     (Common mushroo Basidiomycota;
   PubMed=8662210
                                                                                                AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                               21.9%;
                                                                                                                                                                                                                                                                                                                                                             173531
                                                                                                                               Agaricus
                                                                                                                                    mushroom)
mycota; Hymenomycetes;
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TSP TYPE-1 2.

TSP TYPE-1 3.

TSP TYPE-1 3.

TSP TYPE-1 4.

TSP TYPE-1 4.

TSP TYPE-1 5.

GPS.

GPS.

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POLY-PRO.

POLY-PRO.

POLY-PRO.

CELL ATTACHMENT SITE (POTENTIAL).

NECESSARY FOR INTERACTION WITH BAP1.

INDISPENSABLE FOR INTERACTION WITH BAP1.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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Pred. No. 43;
2; Mismatches
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR EXTRACELULAR (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).
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CYTOPLASMIC (
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7 (POTENTIAL).
                                                                                                                                                                                                                                 PRT;
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                                                                                                   255-277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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                                                                    Thurston C.F.;
                                                                                                   AND
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                                                                                                                                                                                                                                                                                                                      18;
                                                            modular
                                                                                                                                         Homobasidiomycetes,
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                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                            cellulase
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RESULT 13

MPLI_CLUPR

ID MPLI_LOLPR

IO MPL4946; P19964;

AC P14946; P19964;

DT 01-AUG-1991 (Rel.

DT 15-JUN-2002 (Rel.

DE Pollen allergen I
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InterPro; IPRO01524; GH_6.
Pfam; PF00734; CBM_1; 1.
Pfam; PF001341; Glyco_hydro_6; 1.
PRIMTS; PR00733; GLHYDRLASE6.
PRODOm; PD001821; CBD_fungal; 1.
PRODOm; PD00133; GH_G; 1.
SMART; SM00236; fCBD; 1.
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"Correlation of exons with functional
a cellulase from Agaricus bisporus.";
Curr. Genet. 30:56-61(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00562; CBD_FUNGAL; 1.
PROSITE; PS00655; GLYCOSYL_HYDROL_F6_1; 1.
PROSITE; PS00655; GLYCOSYL_HYDROL_F6_2; 1.
Cellulose degradation; Hydrolase; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L24519; AAA50607.1; -.
EMBL; L24520; AAA50608.1; -.
EMBL; Z34007; CAA833971.1; -.
HSSP; P00725; 1AZ6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
VARIANT
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CENTALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic in cellulose and cellotetraose, releasing cellobiose from reducing ends of the chains.
SIMILARITY: BELONGS TO CELLULASE FAMILY B (FAMILY 6 OF G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDROLASES).
SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING
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10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
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NUCLEOPHILE (BY SIMILARITY)
BY SIMILARITY:
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(Rel. 14, Created)
(Rel. 19, Last sequence update)
(Rel. 41, Last annotation update)
rgen Lol p 1 precursor (Lol p I) (

(Allergen

R7)

STANDARD;

PRT;

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EMBL; M57474; AAA63279.1; -.
EMBL; M57476; AAA63378.1; -.
PIR; A23341; A23341.
PIR; B37881; B37881
PIR; B37881; B37881.
PIR; S13614; S13614.
HSSP; P43214; 1WHO.
InterPro; IPR000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen; 1.
PRINTS; PR01225; EXPANSNFAMLY.
PROCOM; PD002179; POLLEn_allergen; 1.
PROCTTE: DS570843; EXPANSIN CRD: 1
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                                                                                                                                                                                                                                                                                                                                                                 This
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Poeae; Lolium.
                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 236-263.
MEDLINE-89364850; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins from rye-grass (Lolium perenne) pollen prepared by a
and efficient purification method.";
Biochem. J. 234:305-310(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cottam G.P., Moran D.M., Standring R.; "Physicochemical and immunochemical characterization of allergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-86242068; PubMed-3718469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rye-grass pollen.";
FEBS Lett. 279:210-215(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Avjoglu A., Davies S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
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                                                                 DOMAIN
                                                                                                      Allergen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Esch R.E., Klapper D.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 24-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91160716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and characterization of a major cross-reactive grass group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knox R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perez M., Ishioka G.Y., Walker L.E., Chesnut R.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                       allergenic determinant.";
ol. Immunol. 26:557-561(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol.
                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Secreted.
DISEASE: CAUSES GRASS POLLEN ALLERGY.
SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
SIMILARITY: CONTAINS 1 EXPANSIN-LIKE E645 DOMAIN.
SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lol p I.";
Chem. 265:16210-16215(1990)
                                                                                                                   PS50842;
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                                                                                                      Glycoprotein;
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                                                                                                                EXPANSIN_CBD;
EXPANSIN_EG45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Lol
                                                                                                      Signal; Multigene
EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
N-LINKED (GLCNAC...
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A -> G.
I -> T.
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                                                                                                      family.
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                                      (POTENTIAL).
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Best Local :
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suphinglu C., Singh M.B., Singson R.J., Ward L., Knox R.:
Suphinglu C., Singh M.B., Singson R.J., Ward L., Knox R.:
"Identification of canary grass (Phalaris aquatica) poll-
by immunoblotting: IgE and IgG antibody-binding studies.
Allergy 48:273-281(1993).
-!- SUBCELLULAR LOCATION: Secreted.
-!- DISEASE: CAUSES GRASS POLLEN ALLERGY.
-!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pollen
Clin. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Major pollen allergen Pha a 1 precursor (Pha a I).
Phalaris aquatica (Canary grass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                     InterPro; IPR000882; Pollen_allergen
pfam; PF01357; Pollen_allergen; 1.
pRINTS; PR01225; EXPANSNFAMLY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, sequencing and expression and four isoforms of Pha a 5, the m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suphioglu C., Singh M.B.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPA1_PHAAQ
Q41260;
                                                               DOMAIN
                                                                                  DOMAIN
                                                                                                                             SIGNAL
                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                               EMBL; S80654; AAB35984.1;
HSSP; P43214; 1WHO.
                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93319091; PubMed=7687099;
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                                                                                                                                              Allergen;
                                                                                                                                                                 PROSITE;
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l2; Conservative
                                                                                                                                                               PS50843; EXPANSIN_CBD; PS50842; EXPANSIN_EG45;
                                                                                                                                              Glycoprotein;
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Last annotation update)
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EXPANSIN-LIKE EG45.
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Pseudomonas aer Bacteria
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P33639;
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Mol. Microb
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                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no rest use by non-profit institutions as as its content modified and this statement is not removed. Usage by an entities requires a license agreement (see http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

Nature 406:99-964(2000)
                                                                                                              PIR;
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STRAIN-ATCC 15692 / PAO1;
MEDLINE-93225810; PubMed-8097014;
Hobbs M., Collie E.S.R., Free P.D., Livingston S.P., Mattick J.S.
"Pils and PilR, a two-component transcriptional regulatory system
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                                       2 WYSWKRSSKSTGLGDTATREGCGPSQSDGCPYNG 35
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SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN
SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIME
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                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                           Z12154; CAA78138.1; -. AE004868; AAG07934.1;
                          PF00512; signal;
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             HATPase_c;
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PROSITE; PS50112; PAS; FALSE_NEG.
Sensory transduction; Transferase; Kinase; Phosphorylation;
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SM00091;
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17; Conserv
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37 PO
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119 P
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PHOSPHORYLATION (AUTO-) (
1F6E0300E2E77A4C CRC64;
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Search completed: January 15, 2003, 08:15:52 Job time: 3.95434 secs

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Result
No.
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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249
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O9vnh0 drosophila
O4428 halocynthia
O9erz0 mus musculu
O9x20 marine prot
Q9f894 marine stro
C53737 streptomyce
O91119 oryza sativ
C93p23 anaplasma m
O9as9 ralstonia s
O9v1x6 drosophila
Q57075 s integron
O9rk46 streptomyce
O9wth6 escherichia
O8qs63 ofimpanzee
O9tyk4 caenorhabdi
Q27183 paramecium
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AE003602; AAF51966.1; .

R EMBL; AV051865; AAF93289.1; .

R FlyBase; FBgn0004878; cas.

R InterPro; IPR000637; AT_hook.

R InterPro; IPR000637; AT_hook.

R InterPro; IPR000822; Znf_C2H2.

R InterPro; IPR000822; Znf_C2H2.

R Pfam; PF00196; Zf-C2H2; 3

R Pfam; PF00096; Zf-C2H2; 3

R SMART; SM00385; AT_hook; 1.

R SMART; SM00385; AT_hook; 1.
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01-JUN-1998
01-JUN-2002
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HRTT-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C. Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wi Yu C., Lewis S.E., Rubin G.M., Celniker S.;
               stage embryos.";
Dev. Genes Evol. 208:164-167(1998)
EMBL; AB009609; BAA24011.1; -.
                                                                                SEQUENCE FROM N.A.
MEDLINE-98267369; PubMed-9601991;
Hotta K., Takahashi H., Satoh N.;
                                                                                                                                                  Stolidobranchia;
NCBI_TaxID=7729;
                                                                                                                                                                                     Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata;
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                                                                "Expression of an ascidian
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                                                                                                                                                                                                                                                                                                                                                                                                            KWHKKRKESLKLGFARFSSSDDCAPAYGEGCAYNWKQT
   P04284; 1CFE.
                                                                                                                                                                                                                                      protein.
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10; Conservative
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3 (TrEMBLrel.
2 (TrEMBLrel.
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                                                                                                                                                                     Pyuridae;
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Last annotation updat
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0; Mismatches
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Nusskern D.R., Pacleb J.M.,
                                                                                                                                                                                                                                                                                                                          415
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1.5;
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                                                                    of.
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InterPro; IPR000884; TSp1.
Pfam; PF00188; SCP; 1.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR00837; V5TPXLIXE.
PRINTS; PR00837; V5TPXLIXE.
PRODOm; PD000542; Allrgn_V5/Tpx1; 1
SMART; SM00198; SCP; 1.
SMART; SM00209; TSp1; 1.
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01-MAR-2001
01-DEC-2001
                                                                                    01-NOV-1999
01-NOV-1999
01-DEC-2001
                                                                                                                                                                                                                                                                                                                         TISSUE-HEAKY;

MEDLINE-21297709; PubMed-11404085;

Yang L.V., Nicholson R.H., Kaplan J., Galy A., Li L.;

"Hemogen is a novel nuclear factor specifically expressed in mouse hematopoietic development and its human homologue EDAG maps to hematopoietic development and its human homologue EDAG maps to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01009; SCP_AG5_PR1_SC7_1; PROSITE; PS01010; SCP_AG5_PR1_SC7_2; PROSITE; PS50092; TSP1; 1.
                                                                 NIFH
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EMBL; AF269248; AAG33367.1; -
MGD; MGI:2136910; Hgn.
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                         marine proteobacterium 'Tomales
Bacteria; Proteobacteria; gamma
                                                                          Nitrogenase
                                                                                                                    Q9x2s0;
                                                                                                                                 Q9x2S0
                                                                                                                                                                                                                                                                           SEQUENCE
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           SEQUENCE FROM
                              NCBI_TaxID=75784;
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16; Conserv
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15; Conserv
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                                                                                    (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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A: 55043 MW;
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Rodentia;
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44.4%;
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TSP1.
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Pred. No.
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Sciurognathi; Muridae;
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                                           subdivision; Vibrionaceae
                                                      Bay med white'
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Matches 12
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SEQUENCE
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PRINTS; PR00091; NITROGNASEII.
PROSITE; PS00746; NIFH_FRXC_1;
PROSITE; PS00692; NIFH_FRXC_2;
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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PRINTS; PR00091; NITROGNASEII.
PROSITE; PS00746; NIFH_FRXC_1;
PROSITE; PS00692; NIFH_FRXC_2;
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"Ubiquity of heterotrophic diazotrophs in mari
submitted (FEB-1988) to the EMBL/GenBank/DDBJ
EMBL; AF046852; AAD23124.1; ...
HSSP; P00459; 1N2C.
Bacteria; Firmicutes; Actinomycetales; Strep NCBI_TaxID=1892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2000) to the EMBL; AF227938; AAG23905.1; HSSP; P00456; ICP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 marine stromatolite eubacterium HB(0898)
Bacteria; environmental samples.
NCBI_TaxID=137314;
                                          Streptomyces lipmanii (Streptomyces alboniger).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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12; Conser
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109 AA;
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109 AA;
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                       Streptomycineae;
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11612 MW;
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38.7%;
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16, L
21, L
Nifh
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ne Bahamian stromatolites.";
EMBL/GenBank/DDBJ databases
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Pred. No. 0.78
4; Mismatches
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Pred. No. 0.78
2; Mismatches
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                     Streptomycetaceae;
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Best Local S
Matches 12
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Q9LI19;
01-OCT-2000 (TrEMBLrel 15, I
01-OCT-2000 (TrEMBLrel 15, I
01-DEC-2001 (TrEMBLrel 19, I
                                                              093P23 PRELIMINARY; PRT; 136 AA. 093P23; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Major surface protein 2 hypervariable region (Fragme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tercero J.A., Espinosa J.C., Lacalle R.A., Jimenez A.;
"The biosynthetic pathway of the aminonucleoside antibiotic Puromycin, as deduced from the molecular analysis of the pur cluster of Streptomyces alboniger";
J. Biol. Chem. 271:1579-1590(1996).
EMBL; 892429; CAA63158.1; -.
HSSP; P80561, 1XJO.
InterPro; IPR003137; PA.
Pfam; PF02225; PA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-ATCC12461;
MEDLINE=96139493; PubMed=8576156;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. Oryza sativa (Rice).
                                  Anaplasmataceae;
                                             Bacteria; Proteobacteria;
                                                         Anaplasma marginale.
                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 316 AA; 3
                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000) to the EMBL; AP001539; BAA92919.1;
                                                                                                                                                                                                                                                                                                                             clone: P0708G02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
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SEQUENCE FROM
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                                                                                                                                                                                     SWRSSNSHSGEGGVSHDDDEAGSGCGEADTDENSSDVNLTSLRPR
                                                                                                                                                                                                         SWKRSSKSTGLG-----DTATREGCGPSQSDGCPYNGRLTTVKPR
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12; Conservative
                                                                                                                                                                                                                                14; Conservative
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                                 Anaplasma
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51358
                                                                                                                                                                                                                                                                              33263 MW;
                                                                                                                                                                                                                                            25.1%;
31.1%;
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                                             alpha
                                                                                                                                                                                                                                                                                                                                                                                                                     Streptophyta; Embryophyta; Tracheophyta;
/ta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                9;
                                                                                                                                                                                                                                Score 62.5; DI
Pred. No. 2.9;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence up
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Pred. No.
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; 15016CCF70E5EBB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                              7D2BFA7A90C9C8B0 CRC64;
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                                            subdivision; Rickettsiales;
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SEQUENCE FROM N.A

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RESOLUTION OF THE CONTRACT OF 
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Best Local
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Best Local
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01-MAY-2000
01-MAR-2002
01-MAR-2002
CG7191 prote
CG7191.
Drosophila me
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01-DEC-2001
01-MAR-2002
                    Eukaryota;
Pterygota;
                                                                                                                                                                                  Q9VLX6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POLYGALACTURONASES).
EMBL; AF417111; AAL24033.1; -.
InterPro; IPR000743; GH28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gonzalez E.T., Allen C.;
"Identifying the role of;
pathogenesis on tomato.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
-I- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ralstonia.
NCBI_TaxID-305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Infect. Immun. 69:5151-5156(2001).
EMBL; AF354475; AAK76937.1; -.
InterPro; IPR002566; Surface_Ag_msp4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      de La Fuente J., Kocan K.M.; "Expression of Anaplasma marginale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00295; Glyco_hydro_28; 1. PROSITE; PS00502; POLYGALACTURONASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-K60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ralstonia solanacearum
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MEDLINE-21340406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell wall;
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                                                                                                                                                                                                                                                                                                          268
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                                                                                                                                                                                                                                                                                                      WWTEKGTKGAYGVVDAST----PSQASGNPNNVDLRTAAP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSKSTGLGDTATREGCGPSQSDGCPYNGRLTTV 40
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13; Conser
                                                                                                   protein.
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136 AA;
                    Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                            melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycosidase; Hydrol
679 AA; 70356 MW;
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ilarity 39.48;
Conservative
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13782 MW;
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ia; beta subdivision; Ralst
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56 MW; 2033B13506E5AA66 CRC64;
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20,
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Last sequence Last anno
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Last sequence update;
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Pred. No.
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59.5;
                                                                                                                                                                                                       PRT;
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annotation update)
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                    Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 679;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                      Q57075 PRELIMINARY;
Q57075;
Q57075;
Q1-NOV-1996 (TrEMBLrel. 01, C
Q1-NOV-1996 (TrEMBLrel. 01, L
Q1-MAR-2002 (TrEMBLrel. 20, L
INTEGRON IN2 FOUND in TN21 (S
                                                                                        dihydropteroate synthase (SUL1), ISTB (ISTB), ISTA (ISTA), TNIBDELTA1) and TNIA (TNIA) genes, complete CDS (SHIGELLA FI.RYMPETT) (ISTB) (TNIBDELTA1) (TNIA).
                                                                                      (ISTB) (TNIBDELTAI
Shigella flexneri,
                Bacteria;
                                 Plasmid IncfII R100
                                                     Escherichia coli
                                                                    unidentified, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20196006; PubMed-10731132;
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                                                                                                                                                                                                                                                                                                                                         209
                                                                                                                                                                                                                                                                                                                                                                            3 YSWKRSSKSTGLGDTATREGCGPSQSD
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                  Proteobacteria;
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                  gamma
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 59;
Pred. No.
                                                                                                                                                                                                                                                  PRT;
                  subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                  Enterobacteriaceae,
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Matches 13
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01-MAY-2000 (TremBLrel.
01-JUN-2002 (TremBLrel.
SEQUENCE FROM N.A.
STRAIN-A3(2);
MEDLINE-97000351; Pubmed-8843436;
Redenbach M., Kieser H.M., Denapa
                                                                                                                                                           STRAIN-A3(2);
Bentley S.D., Parkhill J., I
Submitted (SEP-1999) to the
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         Murphy L., Submitted
                                                                                                                                                                                                                                                                                                                                                                             STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      derivatives.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Submitted (JAN-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=623,
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Brown H.J., Stok
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agship of the floating genome
to the EMBL/GenBank/DDBJ data
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the EMBL/GenBank/DDBJ
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                                                                                                                                                              Barrell B.G., Rajandream M.A
e EMBL/GenBank/DDBJ databases
         Denapaite
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Last sequence update)
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EMBL/GenBank/DDBJ databases
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         Eichner
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         Α.,
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                                                                                                                                                                                           M.A.;
         Cullum
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Best Local
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                                                                                                                                                                                                        Sampei G., Mizobuchi K.;

"Organization and diversification of plasmid gen
nucleotide sequence of the R100 genome.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ da
EMBL; AP000342; BAA78795.1;

InterPro; IPR001584; Rve.
InterPro; IPR002514; Transposase_8.

Pfam; PF00655; Tve; 1.

Pfam; PF01527; Transposase_8; 1.
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STRAIN—83(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Qualil M.A., Kleser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K
warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A set of ordered cosmids and a detailed genetic and the B Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL117669; CAB56138.1;
                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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InterPro; IPR004294; RPE65.
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424
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  WPAWIRRTENAQLTRSMSKKGCSPDNAACEGFFGRLKTELIYPR
                                            WYSWKRSSKSTGLGDTATREGCGPSQSDGCPYNGRLTT--VKPR
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                                                                                        Similarity 29.5
13; Conservative
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                                                                                                                                                                                       Transposase_8;
AA; 59587 MW;
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12, Last sequence update)
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IS1353.
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                                                                                        Score 59; DB Pred. No. 14;
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Pred. No.
                                                                                                                                                                             1.
9984076FB09FE9CA CRC64;
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RESULT 14

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Best Local S
Matches 13
Query Match
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                                                                                                                                                                                               "Direct Submission.";
Submitted (AUG-2001) to the EN
EMBL; AF125461; AAK18995.1; -
InterPro; IPR000884; TSP1.
SMART; SM00209; TSP1; 5.
PROSITE; PS50092; TSP1; 7.
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Q8QS63;
O1-JUN-2002 (TrEMBLrel. 2
O1-JUN-2002 (TrEMBLrel. 2
O1-JUN-2002 (TrEMBLrel. 2
Tegument protein UL25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
COURTNEY L., Langston Y., Drone K., Mead K.;
"The sequence of C. elegans cosmid Y8A9A.";
"The sequence of C. elegans cosmid Y8A9A.";
"The sequence of C. elegans cosmid Y8A9A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Davison A.J., Akter P., Dolan A., Wright K.M., Addison Alcendor D.J., Hayward G.S., McGeoch D.J.;

"The human cytomegalovirus genome revisited.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases

EMBL; AF480884; AAM00675.1; -.

SEQUENCE 682 AA; 75470 MW; 94148CD4C7A584DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science [2]
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 144.3 kDa protein.
Y8A9A.2.
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2; Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID~6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9TYK4
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Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                         Hypothetical protein. SEQUENCE 1360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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   l Similarity
14; Conserv
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Similarity 35.1%;
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Score 59; DB:
Pred. No. 42;
3; Mismatches
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                                                                                                                                             312B206B6D087C3A CRC64;
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Search completed: January 15, 2003, 08:19:25 Job time: 5.96347 secs

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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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9.5 13.2 840 22 AAM23903	0.5 13.2 840 22 ABG01693	3.2 796 23 ABB57294	1.5 13.2 788 22 AAM78375	573.5 13.3 796 15 AAR49730	574.5 13.3 796 22 AAB60418	576 13.3 3028 22 AAE08586	576 13.3 3014 22 AAU02196	576 13.3 3014 22 AAU68533	591 13.7 882 23 AAU78051	591 13.7 882 22 AAB73490	591 13.7 882 21 AAB35730	591 13.7 882 20 AAY09375	591.5 13.7 4643 22 ABB71609	592.5 13.7 117 21 AAY64597	593 13.7 878 23 ABB81475	593 13.7 878 16 AAR85487	593 13.7 878 15 AAR55060	601.5 13.9 3606 22 ABB62595	604 14.0 899 23 ABB81472	605 14.0 4591 22 ABG22977	607 14.0 759 22 ABG21947	611 14.1 4555 23 AAM52106 Rat	630.5 14.6 717 13 AAR27824	630.5 14.6 712 13 AAR27823	657.5 15.2 713 18	657.5 15.2 713 18 AAW25638	665.5 15.4 862 22 AAM41021	667.5 15.4 847 22 AAM39235	671.5 15.5 896 23 AAU78055	671.5 15.5 896 15 AAR63533	684.5 15.8 916 18	.8 916 18 AAW25658	694.5 16.1 906 23 ABB57233	
Human EST encoded	Novel human diagno	Mouse ischaemic co	Human protein SEQ	Sequence encoded b	Mouse PrP-binding		Seven-pass transme	Human novel cytoki	Human E-cadherin p	Human E-cadherin.	Human E-cadherin a	Wild-type E-cadher	Drosophila melanog	Nonclassical cadhe		Human E-cadherin p	Sequence of human	phila melano	Mouse E-cadherin p	Novel human diagno	Novel human diagno	fa		Sequence encoded b	-	Human cadherin-13.	Human polypeptide	Human polypeptide	Human desmocollin	Human HT-1376 cell	Н	Human cadherin-4.	Mouse ischaemic co	

ALIGNMENTS

04-MAY-1999

(first entry)

AAW74089;

AAW74089 standard; Protein; 832 AA.

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RESULT 1
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                                                                                        Alvarez VL,
Omahony DJ,
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Patterson CA,
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                                                                                   Cagney GM,
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The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by creatifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the proteins own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and
                                                                                                                                                                                                                                                                         Ku J,
King '
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10-JAN-2000;
15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
29-JUN-2000;
28-AUG-2000;
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Wang T,
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genic; gene therapy; vaccine; colonic cancer.
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2000US-0480321.
2000US-0504629.
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2000US-0609448.
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Jiang Y
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GENENTECH INC

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AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                   New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
Sequence
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DB; AAA37087.
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Query Match Best Local

21.0%; 30.2%;

Score 908.5; DB 2 Pred. No. 1.1e-64;

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Q Š Š Ω Ş Š В Вþ B 밁 Вþ 밁 δõ В Qy В δÃ ₽ δ 밁 밁 Qγ Best Local Similarity Matches 237; Conserv 643 413 415 528 353 357 293 297 236 237 177 177 117 57 62 LTGE----TDNIFVIERE-GLLYYNRALDRETRSTHNLQVAALDANGIIVEGPVPITIEV QPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTA----TAIDADLEP---AFRLMDFAIERGDTEGTFGLDWEP--DSGHVRLRLCKNLSYEAAPSHE QATDAD-EPFTGSSKIL-YHIIKGDSEGRLGVDTDPHTNTGYVIIK--KPLDFETAAVSN ILLLVLAMDLAGAEGGFSSTCEVEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAML NSIGTLTAHDRDEENTANSFLNYRIVEQTPKLPMDG-LFLIQTYAGMLQLAKQSLKK-QD PLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEVQENERLG STWVSLEPIHLAENLKVLYPHHMAQVHWSGGDVHYHL---ESHPPGPFEVNAEGNLYVTR NIWKAPKPVEMVENSTDPHPIKITQVRWNDPGAQYSLVDKEKLPRFPFSIDQEGDIYVTQ PDMFQLEPRLGALALSPKGSTSLDHALERTYQLLVQVKDMGDQA-SGHQATATVEVSIIE VMYFQINNKTGAISLTREGSQELNPAKNPSYNLVISVKDMGGQSENSFSDTTSVDIIVTE SSVSEFHLILMDVNDNPPRLAKDYTGLFFCHPLSAPGSLIF-EATDDDQHLFRGPHETES TAKDPEGLDISYSLRGDTRGWLKIDHVTGEIFSVAPLD-REAGSPYRVQVVATEVGGSSL IVFKAENPEPLVFGVKYNASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVAIGTKVGNV TPQYNLTIEVSDKD--FKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTNIGSTILTI TEVTRLSAEDADAPGSPNSHVVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLPLRAGQN ELDREAQAEYLLQVRAQNSHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPG VVVVVQSVAKLV-GPGPGPGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLLTI -LTLAPVPSQ------YLCTPRQDHGLIVSGPSKDPDLASGHGP-YSFT Conservative 159; Mismatches 335; Indels 53; Gaps 472 176 647 527 236 176 116 706 642 352 356 235 21;

335;

Indels

53;

Gaps 116

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18-FEB-2000; 2000WO-US04341.

18-FEB-2000; 2000WO-US04342.

22-FEB-2000; 2000WO-US04414.

01-MAR-2000; 2000WO-US05601.

03-MAR-2000; 2000US-0187202.

25-APR-2000; 2000US-0199397.

22-MAY-2000; 2000US-019393.
                                                           The present sequence is a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.
                                         Sequence
                                                                                                                                                                                Claim 12;
                                                                                                                                                                                                       chromosome and gene mapping.
                                                                                                                                                                                                        Eighty four nucleic acids encoding | molecular biology, including use as chromosome and gene mapping. -
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15-SEP-1999;
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                                                                                                                                                                                                                               SEVK
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                                                                                                                                                                                                                                                                              SC-VEGSCFRPAGHQTGIPTVGMAVGILLTTLLVIGIILAVVFIRIKKDKGKDNVESAQA
                                                                                                                                                                                                                                                                                                       LGPNPTVQRDWRLQTLNGSHAYLTLALHWVEPREHIIPVVVSHNAQ--
                                                                                                                                                                                                                                                                                                                                LG-SGSLQNDWEVSKINGTHARLSTRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVTFC
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05-JAN-2000;
06-JAN-2000;
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20-JUL-1999;
26-JUL-1999;
01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
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                               TPQYNLTIEVSDKD--FKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTNIGSTILTI
                                                                                                           NIWKAPKPVEMVENSTDPHPIKITQVRWNDPGAQYSLVDKEKLPRFPFSIDQEGDIYVTQ
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owski PJ, Grimaldi CJ, Gu
MA, Smith V, Stewart TA,
PM, Wood WI;
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Pred. No. 1.1e-64;
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Gurney AL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRO protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; prostate tumoute cell proliferation; necrosis factor-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted protein; PRO; tumour; lung cancer; cancer; prostate tumour; rectal tumour; live
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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2000US-21956P

2000US-22060SP

2000US-220607P

2000US-220634P

2000US-220644P

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2000US-220893P

2000US-220893P

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liver tumour:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Figure 188; 359pp;
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                                 TAIDADLEP---AFRLMDFAIERGDTEGTFGLDWEP--DSGHVRLRLCKNLSYEAAPSHE
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                                                                                                                         TPQYNLTIEVSDKD--FKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTNIGSTILTI
                                                                                                                                                                                                                                                                                                                                                                                                               VMYFQINNKTGAISLTREGSQELNPAKNPSYNLVISVKDMGGQSENSFSDTTSVDIIVTE
IVFKAENPEPLVFGVKYNASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVAIGTKVGNV
                                                                     QATDAD-EPFTGSSKIL-YHIIKGDSEGRLGVDTDPHTNTGYVIIK--KPLDFETAAVSN
                                                                                                        ILLLVLAMDLAGAEGGFSSTCEVEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAML
                                                                                                                                                                           TEVTRLSAEDADAPGSPNSHVVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLPLRAGQN
                                                                                                                                                                                               PLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEVQENERLG
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)B; ABK33629.
                                                                                                                                                                                                                                                ELDREAQAEYLLQVRAQNSHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPG
                                                                                                                                                                                                                                                                                                                    STWVSLEPIHLAENLKVLYPHHMAQVHWSGGDVHYHL---ESHPPGPFEVNAEGNLYVTR
                                                                                                                                                                                                                                                                                                                                                                                          PDMFQLEPRLGALALSPKGSTSLDHALERTYQLLVQVKDMGDQA-SGHQATATVEVSIIE
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C, Gurney
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Smith V, Stephan JF, Watanabe CK, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 908.5; DB 23;
pred. No. 1.1e-64;
59; Mismatches 335;
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Isolated cadherin polypeptide useful for the treatment of central nervous system, cardiovascular, musculoskeletal, gastrointestinal
                                                                                                                                                                                                                                                                                                                   Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                 Cadherin; CDHN-2; nootropic; neuroprotective; cardiant; human; antiinflammatory; gastric; immunostimulant; cytostatic; immunosen Alzheimer's disease; Parkinson's disease; multiple sclerosis; atherosclerosis; angiogenesis; musculoskeletal; ataxia; myotonia; gastrointestinal; gastritis; insulin dependent diabetes mellitus;
                                WPI; 2001-611722/70.
N-PSDB; AAS15602.
                                                                     Curtis RAJ
                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                              cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cadherin-2 (CDHN-2) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU09959;
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                                                                                          (MILL-) MILLENNIUM PHARM INC
                                                                                                                  18-APR-2000;
                                                                                                                                        18-APR-2001;
                                                                                                                                                               25-0CT-2001
                                                                                                                                                                                       WO200179293-A2
                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                          Crohn's disease;
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                                                                                                                  2000US-198466P
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                                                                                                                                                                                                                                                                      540.
                                                                                                                                                                                                                        /note= "Transmembrane
789..813
                                                                                                                                                                                                                                                                                            /note= "signal peptide"
22..830
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                                                                                                                                                         inflammatory; asthma;
                                                                                                                                                                                                              'note-
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                                                                                                                                                                                                              "Transmembrane domain"
                                                                                                                                                                                                                                                                                 "Mature CDHN-2"
                                                                                                                                                                                                                                                           "Transmembrane
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                                                                                                                                                                                                                                                           domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogen;
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gastrointestinal,

inflammatory,

immune

system and cell proliferation

disorders

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a method for producing the CDHN proteins by culturing a transfected host cell line with a vector containing the CDHN proteins and an antibody which selectively binds to the protein. The CDHN proteins and an containing the CDHN proteins and an antibody which selectively binds to the protein. The CDHN proteins may have nootropic, neuroprotective, cardiant, antiinflammatory, gastric, immunostimulant and cytostatic activity and can be used so cadherin-modulators using antisense-therapy or gene-therapy. These proteins are useful for identifying compounds which bind or modulate CDHN-1. The proteins, nucleic acids and antibodies are useful for treating a subject with a disorder characterised by aberrant or unwanted cadherin protein or nucleic acid activity. These disorders include central nervous system (e.g. Alzheimer's disease, parkinson's disease, multiple sclerosis), cardiovascular, (e.g. atherosclerosis, angiogenesis), musculoskeletal (e.g. ataxia, myotonia) gastrointestinal (e.g. gastritis, insulin dependent immune system (e.g. asthma, rheumatoid arthritis, lupus) or cell proliferation disorders (e.g. cancers, leukaemia) and many other conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the cadherin-2 (CDNH-2) protein
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LTIQPSDPMSRTLRFSLVNDSEGWLCIKEVSGEVHTAQSLQGAQPGDTYTVLVEAQDTDK
                                                                                                                     DHKVVVVVSNIEELV-GPGPGPAATATVTILVERVVAPLKLDQESYETSIPVSTPAGSLL
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                                                          GNVTAKDPEGLDISYSLRGDTRGWLKIDHVTGEIFSVAPLD-REAGSPYRVQVVA--TEV
                                                                                                                                                                VSNIVFKAENPEPLVFGVKYNASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVAIGTKV
                                                                                                                                                                                                                                           LVATLMATDADLEP---AFRLMDFAIEEGDPEGIFDLSWEPDSDHVQLRLRKNLSYEAAP
                                                                                                                                                                                                                                                                                TILTIQATDAD-EPFTGSSKIL-YHIIKGDSEGRLGVDTDPHTNTGYVIIKKPLDFETAA
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Pred. No. 3.7e-62;
1; Mismatches 353;
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                                    The patent discloses a method of female primate contraception comprising administering an antagonist of a wnt polypeptide, inhibiting occyte development. Wnt polypeptides are useful for promotive maturation of an immature occyte. Wnt polypeptides are also useful for increasing the number of mature occytes and to enhance occyte viability. Soluble fragments of wnt polypeptides have the ability to inhibit Wnt signalling, e.g., by blocking binding of a naturally-occurring Wnt protein to its receptor. They may be used to generate monoclonal antibodies which can inhibit occyte development. The present sequence is the human N-cadherin. Signal transduction by beta-catenin is mediated by binding to the cytoplasmic domain of a cadherin. Domainant negative mutants of N-cadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human N-cadherin; Wnt antagonist; contraceptive; contraceptive vaccine;
oocyte development; female primate contraception; oocyte viability;
monocional antibody; Wnt signalling.
                                                                                                                                                                                                                                                 Contraceptive composition for inhibiting oocyte development in primate comprises a Wnt polypeptide antagonist
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                           which inhibit Wnt-1 class signals
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Best Local Similarity
   WO200175067-A2
                                                                                                                    Novel human diagnostic protein #14307.
                                                                                                                                                                                                                       ABG14316 standard;
                                   Homo sapiens.
                                                               Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic of
                                                                                                                                                      18-FEB-2002
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                                                                                                                                                                                                                       Protein;
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HAKFLIY--

145

203

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Best Loc Matches

Local

Similarity

210;

Conservative

117 KDINDNRPTFLQSKYEGSVRQNSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLPMINN 176

Indels

103;

21;

VMYFQINNKTGAISLTREGSQELNPAKNPSYNLVISVKDMGGQSENSFSDTTSVDIIV--KDVHEGQP-LLNVKF-----SNCNGKRKVQYESSEPADFKVDEDGMVY--AVRSFPLSSE

-AQDKETQEKWQVAVKLSLKPT--LTEESVKESAEVEEIVFP

144

98

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390

317

SPNMFTINNETGDIITVAAGLDREKVQQYTLIIQATDMEGNPTYGLSNTATAVITVTDVN

MDGLFLIQTYAGMLQLAKQSLKKQDTPQYNLTIEVSDKD-----FKTLCFVQINVIDIN 443

VKDINDNPPTCPSPVTVFEVQENERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTPKLP

389 316

202

-----DQPPTGIFIINPISGQLSVTKPLDREQIARFHLRAHAVDINGNQVENPIDIVIN YSLVDKEKLPRFPFSIDQ-EGDIYVTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVK 329 RQFSKHSGHLQRQKRDWVIP-PINLPENSRGPFPQELVRIRSDRDKNLSLRYSVTGPGA------TENIWKAPKPVEMVENSTDPHPIKITQVRWN------DPGAQ

VIDMNDNRPEFLHQVWNGTVPEGSKPGTYVMTVTAIDADDPNALNGMLRYRIVSQAPSTP

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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical considers involving aberrant protein expression or biological activity. CC imaging of sites expressing (II). (I) and (II) are useful for treating CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed content function, but was obtained in electronic format directly from WIPO as format directly from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
                                                                             Sequence
                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID No 44675; 103pp; English
                                                                             906 AA;
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2000US-0649167
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16.2%; Score 699.5; DB 22 27.4%; Pred. No. 1.3e-47; tive 122; Mismatches 331;
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                                         DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                        New construct encoding soluble cytoplasmic portion of cadherin including beta catenin binding domain useful in treating cancer an associated with high beta-catenin activity e.g. colon cancer an
                                                                                                                                WPI;
                                                                                                                                                                                     (GEIG/)
                                                                                                                     N-PSDB;
                                                                                                                                                                                                                    26-MAY-1998;
26-MAY-1999;
                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                       o-catenin; colon
                                                                                                                                                                                                                                                                                                                                                  Cadherin; alpha-catenin;
                                                                                                                                                                                                                                                                                                                                                                     Human N-cadherin
                                           Example
                                                                                                                                                     Geiger
                                                                                                                                                                                                                                                   17-JUL-2001; 2001US-0905983
                                                                                                                                                                                                                                                                        18-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB81474 standard; Protein;
                                                                                                                                                                           (SADO/)
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                                                                                                                     2002-499105/53
DB; ABN89391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGLGTGAIIAILLCIIILLILVLMFVVWMKRRDKERQAKQLLIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNLKIKFLEAGIYEVPIIITDSGNPPKSNISILRVKVCQCDSNGDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FCHPLSA-----PGSLIFEATDDDQHLFRGPH-FTFSLGSGSLQNDWEVSKINGTHAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTIAVLDRESPNVKNNIYNATFLASDNGIPPMSGTGTLQIYLLDINDNAPQVL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSVAPLDREA----GSPYRVQVVATEVGGSSLSSVSEFHLILMDVNDNPPRLAKDYTGLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPYFAPNPKIIRQEEGLHAGTMLTTFTAQDPDRYMQQNIRYTKLSDPANWLKIDPVNGQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DQIPIF-EKSDYGNLTLAEDTNIGSTILTIQATDADEPFTGSSKILYHIIKGDSEGRLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSTRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVTFCSC-VEGSCFRPAGHQTGIPTV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- PQEAETCETPDPNSINITALDYDIDPNAGPFAFDLPLSPVTIKRNWTITRLNGDFAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --GMAVGILLTTLLVIGIILAVVFIRIKKDKGKDNVESAQASEVKP
                                                                                                                                                    ₽,
                                                                                                                                                                         GEIGER B.
BEN-ZE'EV
SADOT E.
                                         3; Page 45-48; 102pp; English
                                                                                                                                                    Ben-Ze'ev
                                                                                                                                                                                                                                                                                                                                                                                          (first
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99US-0318633
                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                       cancer
                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                    ۶,
                                                                                                                                                                                                                                                                                                                                                                      SEQ
                                                                                                                                                                                                                                                                                                                                               cancer; beta-catenin binding domain; melanoma;
                                                                                                                                                     Sadot
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beta-catenin comprising a gene therapy vehicle harbouring a polynucleotide that contains: (a) a nucleotide sequence encoding an o-catenin; and (b) an upstream promoter for directing expression of the o-catenin in a mammalian cell. The pharmaceutical compositions have cytostatic activity and can be used in the suppression of beta-catenin-mediated transactivation. They can be used for treating cancers associated with abnormally high activity levels of beta-catenin in mammalian cells. The present sequence represents human N-cadherin which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                  polynucleotide that contains: (1) a nucleotide sequence encoding a soluble cytoplasmic portion of a cadherin which lacks a transmembrane portion and an extracellular portion of the cadherin, and includes a beta-catenin binding domain; and (b) an upstream promoter for directin expression of the soluble cytoplasmic portion of the cadherin in a mammalian cell. Also described is a pharmaceutical composition for treating cancer associated with abnormally high activity levels of
Sequence
                                                invention.
906
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 directing
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밁 В 밁 QΥ В Q Query Match Best Local Matches 664 554 494 434 377 444 390 117 728 563 317 330 145 177 Local Sinhes 210; 257 203 271 235 99 47 DTDPHTNTGYVIIKKPLDFETAAVSNIVFKAENPEPLVFGVKYNASSFAKFTLIVTDVNE 562 VKDINDNPPTCPSPVTVFEVQENERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTPKLP KDINDNRPTFLQSKYEGSVRQNSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLPMINN 176 LNLKIKFLEAGIYEVPIIITDSGNPPKSNISILRVKVCQCDSNGDC LSTRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVTFCSC-VEGSCFRPAGHQTGIPTV-TTIAVLDRESPNVKNNIYNATFLASDNGIPPMSGTGTLQIYLLDINDNAPQVL-----APQFSQHVFQAKVSEDVAIGTKVGNVTAKDPEGL---DISYSLRGDTRGWLKIDHVTGEI DQIPIF-EKSDYGNLTLAEDTNIGSTILTIQATDADEPFTGSSKILYHIIKGDSEGRLGV 502 SPNMFTINNETGDIITVAAGLDREKVQQYTLIIQATDMEGIPTYGLSNTATAVITVTDVN VIDMNDNRPEFLHQVWNGTVPEGSKPGTYVMTVTAIDADDPNALNGMLRYRIVSQAPSTP HAKFLIY VMYFQINNKTGAISLTREGSQELNPAKNPSYNLVISVKDMGGQSENSFSDTTSVDIIV--KDVHEGQP-LLNVKF----SNCNGKRKVQYESSEPADFKVDEDGMVY--AVRSFPLSSE 98 FCHPLSA-----PGSLIFEATDDDQHLFRGPH-FTFSLGSGSLQNDWEVSKINGTHAR NPYFAPNPKIIRQEEGLHAGTMLTTFTAQDPDRYMQQNIRYTKLSDPANWLKIDPVNGQI DNPPEFTAMTFYGEV---PENRVDIIVANLTVTDKDQPHTPAWNAVYRISGGDPTGRFAI MDGLFLIQTYAGMLQLAKQSLKKQDTPQYNLTIEVSDKD-----FKTLCFVQINVIDIN 443 -----DQPPTGIFIINPISGQLSVTKPLDREQIARFHLRAHAVDINGNQVENPIDIVIN QTDPNSNDGLVTVVKPIDFETNRMFVLTVAAENQVPLAKGIQHPPQSTATVSVTVIDVNE YSLVDKEKLPRFPFSIDO-EGDIYVTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVK 329 RQFSKHSGHLQRQKRDWVIP-PINLPENSRGPFPQELVRIRSDRDKNLSLRYTVTGPGA-Similarity Conservative -TENIWKAPKPVEMVENSTDPHPIKITQVRWN------DPGAQ 270 16.2%; Score 699.5; DB 227.4%; Pred. No. 1.3e-47; ive 122; Mismatches 331 -AQDKETQEKWQVAVKLSLKPT--LTEESVKESAEVEEIVFP DB 23; 331; Indels Length ----TDVDRIV 103; 906; Gaps 256 144 727 619 433 376 316 785 663 909 675 553 493 389 234 21;

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The present invention describes a pharmaceutical composition for treating cancer associated with abnormally high beta-catenin activity. The pharmaceutical composition comprises a gene therapy vehicle harbouring a

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786 --GMAVGILLTTLLVIGIILAVVFIRIKKDKGKDNVESAQASEVKP

829

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RESULT 11
ABB81471
ID ABB81471
XX ABB811
XX ABB81
XX Cadh
XX C
                                                                                                                                                                                                            The present invention describes a pharmaceutical composition for treating CC cancer associated with abnormally high beta-catenin activity. The CP pharmaceutical composition comprises a gene therapy vehicle harbouring a CC polynucleotide that contains: (1) a nucleotide sequence encoding a CC soluble cytoplasmic portion of a cadherin which lacks a transmembrane CC portion and an extracellular portion of the cadherin, and includes a CC beta-catenin binding domain; and (b) an upstream promoter for directing CC expression of the soluble cytoplasmic portion of the cadherin in a CC mammalian cell. Also described is a pharmaceutical composition for CC treating cancer associated with abnormally high activity levels of EC beta-catenin comprising a gene therapy vehicle harbouring a CC o-catenin; and (b) an upstream promoter for directing expression of the catenin; and (b) an upstream promoter for directing expression of the catenin in a mammalian cell. The pharmaceutical compositions have CC cytostatic activity and can be used in the suppression of the cancers associated with abnormally high activity levels of beta-catenin catenin in mammalian cells. They can be used for treating cancers associated with abnormally high activity levels of beta-catenin catenin in mammalian cells. The present sequence creates thicken N-cadherin which is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                 Query Match
Matches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New construct encoding soluble cytoplasmic portion of cadherin including beta catenin binding domain useful in treating cancer associated with high beta-catenin activity e.g. colon cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cadherin; alpha-catenin;
o-catenin; colon cancer.
                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-499105/53.
N-PSDB; ABN89350, ABN89351.
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(BENZ/) BEN-ZE'EV A.
(SADO/) SADOT E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-1998;
26-MAY-1999;
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                                    Local Similarity
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   Conservative
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99US-0318633
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                             Score 696; DB 23;
Pred. No. 2.6e-47;
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                                                        Length 912;
   Indels 124;
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----TDVDRIVGAGLGTGAIIAILLCIILLILVLMFVVWMKRRDKERQAKQLLIDP
                          PAGHQTGIPTV---GMAVGILLTTLLVIGIILAVVEIRIKKDKGKDNVESAQASEVKP 829
                                                                                                                                                                                                                                                                                                                              RGDTRGWLKIDHVTGEIFSVAPLDREA----GSPYRVQVVATEVGGSSLSSVSEFHLILM 658
                                                                                                    WTIVRISGDHAQLSLRIRFLEAGIYDVPIVITDSGNPHASSTSVLKVKVCQCDINGDC--
                                                                                                                                         WEVSKINGTHARLSTRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVTFCSC-VEGSCFR 774
                                                                                                                                                                                                     DINDNAPQVNPKEAT - - - TCETLQ - PNAINITAVDPDIDPNAGP - FAFELPDSPPSIKRN
                                                                                                                                                                                                                                                     DVNDNPPRL-AKDYTGLFFCHPLSAPGSLIFEATDDDQHLFRGPHFTFSLGSG--SLQND 715
                                                                                                                                                                                                                                                                                                       LSDPANWLKIDPVNGQITTTAVLDRESIYVQNNMYNATFLASDNGIPPMSGTGTLQIYLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVAIGTKVGNVTAKDP----EGLDISYSL 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARYQMTGGDPTGQFTILTDPNSNDGLVTVVKPIDFETNRMFVLTVAAENQVPLAKGIQHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSFLNYRIVEQTPKLPMDGLFLIQTYAGMLQLAKQSLKKQDTPQYNLTIEVSDKD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVNGNQVENPIDIVINVIDMNDNRPEFLHQVWNGTVPEGSKPGTYVMTVTAIDADDPNAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SDRDKSLSLRYSVTGPGADQPPTGIFIINPISGQLSVTKPLDREQIASFHLRAHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QYSLVDKEKLPRFPFSI-----DQ------EGDIYVTQPLDREEKDAYVFYAVAK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKDQKKIEDIIFPWQQYKDSSHLKRQKRDWVIP-PINLPENSRGPFPQELVRIR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -FKTLCFVQINVIDINDQIPIF-EKSDYGNLTLAEDTNIGSTILTIQATDADEPFTGSSK 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDFRYGEDGVYYAERSFQLSAEPTE----FVVSARDKETQEEWQMKVKLTPEPAFTGAS
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RESULT 12
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ID ABB57
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XX WO200
XX Y AB50
PN WO200
XX Y 18-MA
18-MAY-2001; 2001WO-JP04192
                         22-NOV-2003
                                                WO200188188-A2
                                                                        Mus musculus
                                                                                             Mouse; ischaemia; compressive ischaemia; occassospastic ischaemia; ischaemic condition;
                                                                                                                                  Mouse ischaemic condition related protein sequence SEQ
                                                                                                                                                          07-MAR-2002
                                                                                                                                                                                  ABB57233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a cgene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive consciously considered for a schaemia, occlusive ischaemia or vasospastic ischaemia) by measuring cexpression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the cexpression profile of a gene group comprising these genes. The cused as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB19913 and AB19914 crepresent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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YFAPNPKIIRQEEGLHAGTMLTTLTAQDPDRYMQQNIRYTKLSDPANWLKIDPVNGQITT
                                                                                                  DPHTNTGYVIIKKPLDFETAAVSNIVFKAENPEPLVFGVKYNASSFAKFTLIVTDVNEAP
                                                                                                                                                                                                                                                                                                                                                 ----DQPPTGIFIINPISGQLSVTKPLDRELIARFHLRAHAVDINGNQVENPIDIVINVI
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                                          QFSQHVFQAKVSEDVAIGTKVGNVTAKDPEGL---DISYSLRGDTRGWLKIDHVTGEIFS
                                                                                                                                               PPEFTAMTFYGEV---PENRVDVIVANLTVTDKDQPHTPAWNAAYRISGGDPTGRFAILT
                                                                                                                                                                               IPIF-EKSDYGNLTLAEDTNIGSTILTIQATDADEPFTGSSKILYHIIKGDSEGRLGVDT
                                                                                                                                                                                                                NMFTINNETGDIITVAAGLDREKVQQYTLIIQATDMEGNPTYGLSNTATAVITVTDVNDN
                                                                                                                                                                                                                                              GLFLIQTYAGMLQLAKQSLKKQDTPQYNLTIEVSDKD-----FKTLCFVQINVIDINDQ 445
                                                                                                                                                                                                                                                                                  DMNDNRPEFLHQVWNGSVPEGSKPGTYVMTVTAIDADDPNALNGMLRYRILSQAPSTPSP
                                                                                                                                                                                                                                                                                                              DINDNPPTCPSPVTVFEVQENERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTPKLPMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VMYFQI---NNKTG----AISLTREGSQELNPAKNP-SYNLVISVKDM---GGQSENSF
                                                                           DPNSNDGLVTVVKPIDFETNRMFVLTVAAENQVPLAKGIQHPPQSTATVSVTVIDVNENP
                                                                                                                                                                                                                                                                                                                                                                                 LVDKEKLPRFPFSIDQ-EGDIYVTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVKVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 694.5; DB 2
Pred. No. 3.4e-47;
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RESULT 13
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           This sequence represents human cadherin-4. The invention specifically c provides details of human cadherin-5, -8, -11, -12 and -13, and rat cadherin-8, -5, -11 and -13. Cadherins are calcium-dependent cell adhesion proteins. They are glycosylated integral membrane proteins that have an N-terminal extracellular domain that determines binding specificity, a hydrophobic membrane spanning region and a C-terminal cytoplasmic domain, which is highly conserved among members of the superfamily. The C-terminal domain interacts with the cytoskeleton through eatenins and other cytoskeleton-associated proteins. The coadherin proteins may be used in the analysis of the role of cadherin. The cadherin proteins may be isolated by using anti-cadherin cadherin. The cadherin proteins may be isolated by using anti-cadherin also allows investigation of the structure and function of cadherin. The cadherin proteins may be isolated by using anti-cadherin may be used to modulate the activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                    19-APR-1993;
17-APR-1992;
01-NOV-1994;
 of cadherin and to
                                                                                                                                                                                                                                                                                                                                                                         Suzuki
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                                                                                                                                                                                                                                                          Example
                                                                                                                                                                                                                                                                                      Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion
                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT85433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-1992;
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                                                                                                                                                                                                                                                          2; Column 61-66; 56pp;
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92US-0872643.
94US-0332638.
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determine the tissue specific
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o modulate the activity distribution of cadherin
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RESULT 14
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Best Local Similarity
Matches 176; Conserv
                                                                                                                                Ca2+ dependent; cell adhesion protein; foetal; cadherin; brain; human; antibody; purification; determination; tissue expression; binding antagonist; calcium ion.
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  28-JAN-1997
                                                                                         Homo sapiens
                                                                                                                                                                                                                                Full length
                                                                                                                                                                                                                                                                                 13-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 WKAPKPVEMVENSTDPHPIKITQVRW---NDPGAQYSL--VDKEKLPRFPFSID-QEGDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    528 TFSAVDPDRFMQQAVRYSKLSDPASWLHINATNGQITTVAVLDRESLYTKNNVYEATFLA
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                                                                                                                                                                                                                                   human
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Best Local
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17-APR-1992;
19-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is full length human cadherin-4, whi is a Ca2+ dependent cell adhesion protein. The human cadh was isolated from a foetal brain cDNA library, using prob on homologous rat cadherin cDNA.

Antibodies or fragments that specifically bind the human can be used to purify the cadherin, determine its tissue and antagonise its ligand/antiligand binding activities.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibodies to cadherin proteins - useful as cadherin antagonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-108328/10.
N-PSDB; AAT61920.
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                        IIKVKVCPCDDNGDCTTIG---AVAAAGLGTGAIVAILICILILLTMVLLFVMWMKRREK
                                                SLPVTFCSCVEGSCFRPAGHQTGIPTVGMAVGILLTTLLVIGIILAVV--FIRIKKDKGK 816
                                                                                                                                                                                                                                                                                                    TFSAVDPDRFMQQAVRYSKLSDPASWLHINATNGQITTVAVLDRESLYTKNNVYEATFLA
                                                                                                                                                                                                                                                                                                                                                NVTAKDPEGL---DISYSLRGDTRGWLKIDHVTGEIFSVAPLDREA----GSPYRVQVVA
                                                                                                                                                                                                                                                                                                                                                                                             FMLTVMVSNQAPLASGIQMSFQSTAGVTISIMDINEAPYFPSNHKLIRLEEGVPPGTVLT
                                                                                                                                                                                                                                                                                                                                                                                                                        SNIVFKAENPEPLVFGVKYNASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVAIGTKVG 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVVANLTYMDRDQPHSPNWNAVYRIISGDPSGHESVRTDPVTNEGMVTVVKAVDYELNRA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STILTIQATDADEPFTGSSKILYHIIKGDSEGRLGVDTDPHTNTGYVIIKKPLDFETAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKPGTYVMTITANDADDSTTANGMVRYRIVTQTPQSPSQNMFTINSETGDIVTVAAGWDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTPKLPMDGLFLIQTYAGMLQLAKQSLKK 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YVTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEVQEN 352
                                                                                                               GPYVFELPFVPAAVRKNWTITRLNGDYAQLSLRILYLEAGMYDVPIIVTDSGNPPLSNTS
                                                                                                                                    GPH-FTFSLGSGSLQNDWEVSKINGTHARLSTRHTDFEERAYVVLIRINDGGRPPLEGIV
                                                                                                                                                                                                           ADNGIPPASGTGTLQIYLIDINDNAPELLPKEAQICERPNLNA---INITAADADVHPNI 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKVQQYTVIVQATDMEGNLNYGLSNTATAIITVTDVNDNPSEFTASTFAG--EVPENSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDTPQYNLTIEVSDKD-----FKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTNIG 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YVTRPMDREEHASYHLRAHAVDMNGNKVENPIDLYIYVIDMNDNHPEFINQVYNCSVDEG
                                                                                                                                                                                                                                                      TEVGGSSLSSVSEFHLILMDVNDNPPRLAKDYTGLFFCHPLSAPGSLIFEATDDDQHLFR
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93US-0049460.
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                                                                                                                                                                                                                                                                                              Query Match 15.5
Best Local Similarity 30.8
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences coding for proteins having monocyte and macrophage migration factor activity were isolated from a cDNA library prepared from human HT-1376 cells (ATCC CRL-1472). The proteins encoded by the isolated cDNA clones are useful as immunopotentiators for treatment of infections, immune deficiency diseases and cancer. The proteins are also useful in wound healing preparations and for treatment of skin diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 34-41; 68pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monocyte and macrophage migration factor protein immuno-potentiator and vulnerary and is isolated HT-1376 cell line by recombinant methods
                                                                                                                                                                                                 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ72597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawamura K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human HT-1376 cell-derived Leukocyte Chemotactic Factor.
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VLESSRPGTTVGVVCATDRDEPDTMHTRLKYSILQQTPRSP--GLFSVHPSTGVITTVSH
                              NLFCTRPVDREEYDVFDLIAYASTADGYSADL--PLPLPIRVEDENDNHPVFTEAIYNFE
                                                                                                                             DIYVTQPLDREEKDAY--VFYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFE
                                                                                                                                                                                            W-APIPCSMQENSLGPFPLFLQQVE-SDAAQNYTVFYSISGRGVDKEPLNLFYIERD-TG
                                                                                                                                                                                                                                WKAPKPVEMVENSTDPHPIKITQVRWNDPGAQYSL-----VDKEKLPRFPFSIDQEG
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Pred. No. 2.5e-45;
)6; Mismatches 263;
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                           IKKDKGK
                                                                                                                                                                                                RPPLEGIVSLPVTFCSCVEGSCFRPAGHQTGIPTVGMAV-GILLTTLLVIGIILAVVFIR
                                                                                                                                                                               NITVLAIDKDDRSCTGTLAVN--IEDVNDNPPEILQEY--VVICKPKMGYTDIL--AVDP
                                                                                                                                                                                                                                        VGSKINGYKAYDPENRNGNGLRYKKLHDPKGWITIDEISGSIITSKILDREVETPKNELY
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                                                      RAGQAATKLLRVNLCECTHPTQCRATSRSTGVILGKWAILAILLGIALLESVLLTLVCGV
                                                                                                                     DEPVHGAP-FYFSLPNTSPEISRLWSLTKVNDTAARLSYQKNAGFQE--YTIPITVKD--
                                                                                                                                                                                                                                                                                                                                    ETAAVSNIVFKAENPEPLVFGV-KYNASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVA
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Result
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptcodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptcodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptcodata/1/pubpaa/US06_NEW_PUB.pep:*

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11: /cgn2_6/ptcodata/1/pubpaa/US09_NEW_PUB.pep:*

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13: /cgn2_6/ptcodata/1/pubpaa/US09_NEW_PUB.pep:*

14: /cgn2_6/ptcodata/1/pubpaa/US09_NEW_PUB.pep:*
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1 MILQAHLHSLCLLMLYLATG.....DKGKDNVESAQASEVKPLRS
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US-09-933-263-1081
US-09-933-263-1087
US-09-933-263-1087
US-09-933-263-1087
US-10-063-547-98
US-10-06-867-98
US-10-06-867-98
US-09-905-983-26
US-09-905-983-26
US-09-905-983-26
US-09-746-491-46
US-09-746-491-47
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Compugen Ltd
          Sequence 1081, Ap
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Sequence 1087, Ap
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Sequence 1087, Ap
Sequence 98, Appl
Sequence 98, Appl
Sequence 46, Appl
Sequence 2, Appli
Sequence 44, Appl
Sequence 49, Appl
Sequence 49, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xu, Jiangchun
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Lodes, Michael J

ALIGNMENTS

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APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1081
                                                                                                                                                            ; ORGANISM: Homo sapiens US-10-025-380-1081
                                                                            Query Match
Best Local Similarity
Matches 832; Conserv
                                                                                                                                                                                                LENGTH: 832
TYPE: PRT
                     1 MILQAHLHSLCLLMLYLATGYGQEGKFSGPLKPMTFSIYEGQEPSQIIFQFKANPPAVTF
MILQAHLHSLCLLMLYLATGYGQEGKFSGPLKPMTFSIYEGQEPSQIIFQFKANPPAVTF
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Smith, Carole L.
King, Gordon E.
Wang, Aijun
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Stolk, John A.
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Benson, Darin R.
                                                                              Conservative
                                                                                               100.0%;
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                                                                          Score 4321; DB 9;
Pred. No. 4.1e-316;
); Mismatches 0;
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RESULT 2
US-09-922-217-1081
US-09-922-217-1081
Sequence 1081, Application US
Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael CAPPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R
APPLICANT: Meagher, Madele:
APPLICANT: Weagher, Madele:
APPLICANT: Stolk, John A
APPLICANT: Smith, Carole Ly
APPLICANT: Smith, Carole Ly
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Clapper, Jonath
TITLE OF INVENTION: COMPOUNI
TITLE OF INVENTION: OF COLA
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LICANT: Meagher, Madeleine J
LICANT: Stolk, John A.
LICANT: Stolk, John A.
LICANT: Jiang, Yuqiu
LICANT: Jiang, Yuqiu
LICANT: Smith, Carole Lynn
LICANT: King, Gordon E.
LICANT: Wang, Aijun
LICANT: Clapper, Jonathan D.
LICANT: Clapper, Jonathan D.
LICANTION: COMPOUNDS FO
LE OF INVENTION: OF COLON CA
E REFERENCE: 210121.471C13
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                                                                                                         Secrist, Heather
Benson, Darin R.
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FOR IMMUNOTHERAPY AND DIAGNOSIS
CANCER AND METHODS FOR THEIR USI
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; ORGANISM: Homo
US-09-922-217-1081
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Best Local s
Matches 832
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CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Ves
SEQ ID NO 1081
LENGTH: 832
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       GIPTVGMAVGILLTTLLVIGIILAVVFIRIKKDKGKDNVESAQASEVKPLRS
                              INGTHARLSTRHIDFEERAYVVLIRINDGGRPPLEGIVSLPVTFCSCVEGSCFRPAGHQT
                                                            NDNPPRLAKDYTGLFFCHPLSAPGSLIFEATDDDQHLFRGPHFTFSLGSGSLQNDWEVSK
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Pred. No. 4.1e-316;
Mismatches 0;
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US-09-833-263-1081

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Sequence 1081, Application US/09833263
Patent No. US20020110547A1
GENERAL INFORMATION:
APPLICANT: Wang, Aljun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Modeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METITIE REFERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1081
LENGTH: 832
TYPE: PRT
ORGANISM: Homo sapiens
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                        NDNPPRLAKDYTGLFFCHPLSAPGSLIFEATDDDQHLFRGPHFTFSLGSGSLQNDWEVSK
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INGTHARLSTRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVTFCSCVEGSCFRPAGHQT
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Pred. No. 4.1e-316;
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CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 1087
LENGTH: 958
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                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 813; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Fanger, Garry R.
APPLICANT: Vedvick Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
TILE REFERENCE: 210121.471C14
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              SFLNYRIVEQTPKLPMDGLFLIQTYAGMLQLAKQSLKKQDTPQYNLTIEVSDKDFKTLCF 434
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                                                       EYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEVQENERLGNSIGTLTAHDRDEENTAN
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Secrist, Heather
Benson, Darin R.
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Smith, Carole L.
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Stolk, John A.
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99.48;
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Pred. No. 1.5e-307;
1; Mismatches 2;
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APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Mang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Yuqiu
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Wang, Ajun
APPLICANT: Wang, Ajun
APPLICANT: Wang, Ajun
APPLICANT: Wang, Ajun
APPLICANT: HORE COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEG ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1087
LENGTH: 958
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US-09-922-217-1087
; Sequence 1087, Application US/09922217
; Patent No. US20020076414A1
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VRQNSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLPMINNVMYFQINNKTGAISLTRE
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                                           EGLLYYNRALDRETRSTHNLQVAALDANGIIVEGPVPITIEVKDINDNRPTFLQSKYEGS
                                                                                  LASGSAAAQEGKFSGPLKPMTFSIYEGQEPSQIIFQFKANPPAVTFELTGETDNIFVIER
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                                                                                                                                           Conservative
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99.4%;
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Pred. No. 1.5e-307;
1; Mismatches 2;
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GENERAL INC. USACCELLARY GENERAL INFORMATION:
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND FILE REFERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1087
LENGTH: 958
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-833-263-1087
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           Score 4208;
Pred. No. 1
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      APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ell
APPLICANT: Filvaroff, Ell
APPLICANT: Gorritsen, Mar
APPLICANT: Goddward, Audre
APPLICANT: Goddward, Paul
APPLICANT: Grimaldi, Chri
APPLICANT: Grimaldi, Chri
APPLICANT: Watanabe, Coli
APPLICANT: Wood, William
APPLICANT: Wood, William
                                                                                                     Sequence 98, Application US/10063547 Publication No. US20020182638A1 GENERAL INFORMATION:
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 INVENTION:
        Filvaroff, Ellen
Gerritsen, Mary E.
Goddard, Audrey
Goddwski, Paul J.
Grimaldi, Christopher J
Grimaldi, Christopher J
Gurney, Austin L.
Watanabe, Colin K.
Watanabe, Tolin M.
Wood, William I.
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CURRENT APPLICATION UNMERR: US/10/063,547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapp NUMBER OF SEQ ID NOS: 170
SEQ ID NO 98
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RESULT 8
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OR FILING DATE: 1999-04-13
OR APPLICATION NUMBER: 60/129674
OR FILING DATE: 1999-04-16
OR APPLICATION NUMBER: 60/131291
OR FILING DATE: 1999-04-27
OR APPLICATION NUMBER: 60/138387
OR FILING DATE: 1999-06-09
OR APPLICATION NUMBER: 60/144791
OR FILING DATE: 1999-07-20
OR APPLICATION NUMBER: 60/169495
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OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/113430
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OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/115614
OR FILING DATE: 1999-12-30
OR APPLICATION NUMBER: 60/116527
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OR FILING DATE: 1999-01-20
OR APPLICATION NUMBER: 60/116843
OR FILING DATE: 1999-01-22
OR APPLICATION NUMBER: 60/119285
OR FILING DATE: 1999-02-09
OR APPLICATION NUMBER: 60/119287
OR APPLICATION NUMBER: 60/119287
OR FILING DATE: 1999-02-09
OR APPLICATION NUMBER: 60/119287
OR FILING DATE: 1999-02-09
OR APPLICATION NUMBER: 60/119525
OR FILING DATE: 1999-02-10
OR APPLICATION NUMBER: 60/119549
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                                   VMYFQINNKTGAISLTREGSQELNPAKNPSYNLVISVKDMGGQSENSFSDTTSVDIIVTE
PDMFQLEPRLGALALSPKGSTSLDHALERTYQLLVQVKDMGDQA-SGHQATATVEVSIIE
                                                                                 KDENDQVPHFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPS
                                                                                                         KDINDNRPTFLQSKYEGSVRQNSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLPMINN
                                                                                                                                                                  LSGDSGKATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHV 116
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                                                                    Query Match
Best Local Sim
Matches 245;
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TITLE OF INVENTION: 57809 AND 57798, NOVEL HUMAN CADHERIN
TITLE OF INVENTION: MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-145
CURRENT APPLICATION NUMBER: US/09/838,529
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/198,466
PRIOR APPLICATION NUMBER: 60/198,466
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                              LENGTH: 830
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LSGDSNTADQNTFAVDTDSGFLVATRTLDREEKAEYQLQVTLESEDGRILWGPQLVTVHV 118
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                                                                                       Similarity
                                                                      Conservative
                                                                                       20.3%;
                                                                    %; Score 877.5; DB 1
%; Pred. No. 8.6e-58
141; Mismatches 35
                                                                                                         DB 10;
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Sequence 46, Application US/09905983
Patent NO. US20020045591A1
GENERAL INFORMATION:
APPLICANT: Gelger, Benjamin
APPLICANT: Ben-Ze'ev, Avri
APPLICANT: Sadot, Einat
TITLE OF INVENTION: METHODS AND THERAPEUTIC CONFILE REFERENCE: 01/22326
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
; ORGANISM: Homo sapiens US-09-905-983-46
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                             --GMAVGILLTTLLVIGIILAVVFIRIKKDKGKDNVESAQASEVKP 829
                                                                                              LSTRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVTFCSC-VEGSCFRPAGHQTGIPTV-
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RESULT 11
US-09-905-983-2
; Sequence 2, Application US/09905983
; Patent No. US20020045591A1
; Patent No. US20020045591A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Geiger, Benjamin
APPLICANT: Ben-Ze'ev, Avri
APPLICANT: SAGOt, Einat
TITLE OF INVENTION: METHODS AND THERAPEUTIC COMPOSITIONS FOR TREATING CANCER
FILE REFERENCE: 01/23326
; CURRENT APPLICATION NUMBER: US/09/905,983
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2

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RESULT 12
US-09-746-491-46
US-09-746-491-46
Sequence 46, Application US/09746491
Patent No. US20020137202A1
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
ITILE OF INVENTION: No. US20020137202A1e1 Proteins and FILE REFERENCE: 15966-621
CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
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US-09-905-983-2
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TYPE: PRT
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Pred. No. 4.1e-44;
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NUMBER OF SEQ ID NOS: 72
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 46
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                                                           IVGAGLGTGAIIAILLCIIILLILVLMFVVWMKRRDKERQAKQLLIDP
                                                                                        V---GMAVGILLTTLLVIGIILAVVFIRIKKDKGKDNVESAQASEVKP 829
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                                                                                                                      AQLNLKIKFLEAGIYEVPIIITDSGNPPKSNISILRVKVCQCDSNGDC-----
                                                                                                                                                  ARLSTRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVTFCSC-VEGSCFRPAGHQTGIPT
                                                                                                                                                                                  ----PQEAETCETPDPNSINITALDYDIDPNAGPFAFDLPLSPVTIKRNWTITRLNGDF
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Sequence 49, Application US/09746491 Patent No. US20020137202A1 GENERAL INFORMATION: APPLICANT: Burgess, Catherine E. APPLICANT: No. US200201372

Catherine E. No. US20020137202Alel Proteins and Nucleic Acids Encoding

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US-09-746-491-49
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CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 49
SEQ ID NO 49
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TYPE: PRT
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                              FRPAGHQTGIPTV---GMAVGILLTTLLVIGIILAVVFIRIKKDKGKDNVESAQASEVKP
                                                                                             NDWEVSKINGTHARLSTRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVTFCSC-VEGSC
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                                                              RNWTIVRISGDHAQLSLRIRFLEAGIYDVPIVITDSGNPHASSTSVLKVKVCQCDINGDC
                                                                                                                                                                                            SKLSDPANWLKIDPVNGQITTTAVLDRESIYVQNNMYNATFLASDNGIPPMSGTGTLQIY
                                                                                                                                                                                                                                                           HPPQSTATVSITVIDVNESPYFVPNPKLVRQEEGLLAGSMLTTFTARDPDRYMQQTSLRY
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----TDVDRIVGAGLGTGAIIAILLCIIILLILVLMFVVWMKRRDKERQAKQLLIDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -WKAPKPVEMVENSTDPHPIKITQVRWNDPGA
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RESULT 14 US-09-746-491-48

Sequence 48,

Application US/09746491

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 48
LENGTH: 906
LENGTH: 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. US20020137202A1
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine
TITLE OF INVENTION: No. US2002
FILE REFERENCE: 15966-621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                 APQFSQHVFQAKVSEDVAIGTKVGNVTAKDPEGL---DISYSLRGDTRGWLKIDHVTGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VMYFQI----NNKTG-----AISLTREGSQELNPAKNP-SYNLVISVKDM----GGQSENSF
GAGLGTGAIIAILLCIILLILVLMFVVWMKRRDKERQAKQLLIDP
                              --GMAVGILLTTLLVIGIILAVVFIRIKKDKGKDNVESAQASEVKP
                                                                                                  LSTRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVTFCSC-VEGSCFRPAGHQTGIPTV-
                                                                                                                                      ---PQEAETCETPEPNSINIAALDYDIDPNAGPFAFDLPLSPVTIKRNWTINRLNGDFAQ
                                                                                                                                                                           FCHPLSA-----
                                                                                                                                                                                                             TTIAVLDRESPYVQNNIYNATFLASDNGIPPMSGTGTLQIYLLDINDNAPQVL-----
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; TYPE: PRT
; ORGANISM: BOS taurus
US-09-746-491-47
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US-09-746-491-47
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Patent No. US20020137202A1
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: No. US20020137202A1e1 Proteins and Nucleic Acids Encoding Same
FILE REPERENCE: 15966-621
CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
COURTENT FILING DATE: 2000-12-20
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PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 47
SEQ ID NO 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 203; Conserv
    640 KFLEAGIYEVPIIITDSGNPPKSNISILRVKVCQCDSNGDC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 FLQSKYEGSVRQNSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLP------MINN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                    444 DQIPIFEKSD---YGNLTLAEDTNIGSTILTIQATDADEPFTGSSKILYHIIKGDSEGRL 500
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                             TDFEERAYVVLIRINDGGRPPLEGIVSLPVTFCSC-VEGSCFRPAGHQTGIPTV---GMA 788
                                                                                                                        LFFCHPLSAPGSLIFEATDDDQHLFRGPH-FTFSLGSGSLQNDWEVSKINGTHARLSTRH 732
                                                                                                                                                              EIFSVAPLDREA----GSPYRVQVVATEVGGSSLSSVSEFHLILMDVNDNPPRLAKDYTG 673
                                                                                                                                                                                                                                              NENPYFAPNPKIIRQEEGLHAGTVLTTFTAQDPDRYMQQNIRYTKLSDPANWLKIDSVNG
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                                                                                I--CE-TPDPNSINITALDYDIDPNAGPFAFDLPLSPVTIKRNWTITRLNGDFAQLNLKI 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DQPPTGIFIINPISGQLSVTKPLDRELIARFHLRAHAVDINGNQVENPIDIVIN 227
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Conservative 126;
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---TDVDRIVGAGLG 692
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Qy 789 VGILLTTLLVIGIILAVVFIRIKKDKGKDNVESAQASEVKP 829
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Db 693 TGAIIAILLCIIILLILVLMEVVWMKRRDKERQAKQLLIDP 733
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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2: pir2:*
3: pir3:*
4: pir4:*
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C;Bate: 15-Uul-1995 #sequence_revision 01-Sep-1995 #text_change
C;Bate: 15-Uul-1995 #sequence_revision 01-Sep-1995 #text_change
C;Accession: S5396
R;Boettinger, A.; Kreft, B.; Fieger, C.; Dlouhy, B.; Berndorff,
submitted to the EMBL Data Library, December 1994
A;Description: Molecular cloning of human LI-cadherin:evidence
A;Reference number: S5396
A;Reference number: S5396
A;Accession: S5396
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-832 <BOE>
A;Accession: S5396
A;Accession: S
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IJMSCP
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Pred. No. 1.3e-262;
2; Mismatches 2;
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Minimum Maximum

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LI-cadherin precursor - rat
LI-cadherin precursor - rat
N;Alternate names: liver-intestine cadherin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 31-N
C;Accession: A53954
R;Berndorff, D.; Gessner, R.; Kreft, B.; Schnoy, N.; Lajous-Petter,
J. Cell Biol. 125, 1353-1369, 1994
A;Title: Liver-intestine cadherin: molecular cloning and characteriz
A;Reference number: A53954; MUID:94266966; PMID:8207063
A;Reference number: A53954
A;Status: preliminary
A;Cccssion: A53954
A;Residues: 1-827 < ABER>
A;Cccss-references: GB:X78997; NID:9505562; PIDN:CAA55631.1; PID:950562; Superfamily: cadherin; cadherin repeat homology
C;Keywords: calclum binding; cell adhesion; duplication; glycoprote: F:1-28/Domain: signal sequence #status predicted <MAT>
F:454-565/Domain: cadherin repeat homology <CR3>
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        PKPVEMVENSTDPHPIKITQVRWNDPGAQYSLVDKEKLPRFPFSIDQEGDIYVTQPLDRE

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78.8%; Pred. No. 1e-206;
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Ksp-cadherin - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_ch
C;Accession: 146536
R;Thomson, R.B.; Igarashi, P.; Biemesderfer, D.; Kim, R.; A
J; Biol. Chem. 270, 17594-17601, 1995
A;Title: Isolation and cDNA cloning of Ksp-cadherin, a nove
A;Reference number: 146536; MUID:95340560; PMID:7615566
A;Accession: 146536
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-829 <THO>
A;Cross-references: EMBL:U28945; NID:g902885; PIDN:AAC4847;
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                                                  KDINDNRPTFLQSKYEGSVRQNSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLPMINN
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              NIWKAPKPVEMVENSTDPHPIKITQVRWNDPGAQYSLVDKEKLPRFPFSIDQEGDIYVTQ : | : | : | | : | | : | | : | | : | | |
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STWTPLEPVHLAENLKVPYPHHLAQVHWSGGDVHYRL--
                                                                                                       KDENDQVPQFSQALYSARLSQGTRPGVPFLFLEASDGDEPGTANSDLRFHILSQTPAQPS
                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                               EMBL: U28945; NID: g902885; PIDN: AAC48472.1;
                                                                                                                                                                                                                       22.1%;
                                                                                                                                                                                                           Score 954; DB 2;
Pred. No. 5.7e-52;
2; Mismatches 354
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 ESQPPGPFDVDTEGKLYVTG
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R-cadherin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Jun-2000
C;Accession: JH0424
R;Inuzuka, H.; Miyatani, S.; Takeichi, M.
Neuron 7, 69-79, 1991
                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: JH0424; A; Accession: JH0424
                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: R-cadherin: a novel Ca2+-dependent cell-cell adhesion A; Reference number: JH0424; MUID:91299341; PMID:1712604
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RESULT 5
A47543
A-7543
R-cadherin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C;Accession: A47543; I55501
R;Hutton, J.C.; Christofori, G.; Chi, W.Y.; Edman, U.; Guest, P.C.; Hanahan, D.;
Mol. Endocrinol. 7, 1151-1160, 1993
A;Title: Molecular cloning of mouse pancreatic islet R-cadherin: differential e)
A;Reference number: A47543; MUID:94067164; PMID:8247017
A;Accession: A47543
A;Accession: A47543
A;Residues: 1-913 <HUID-
A;Cross-references: EMBL:X69966; NID:9429111; PIDN:CAA49589.1; PID:9429112
R;Matsunami, H.; Miyatani, S.; Inoue, T.; Copeland, N.; Gilbert, D.; Jenkins, N
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Best Local Similarity
Matches 203; Conserv
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                                                                              AIYRIISGDPSGHFTIRTDPVTNEGMVTVVKAVDYEMNRAFMLTVMVSNQAPLASGIQMS
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   TTIG---
                              RPAGHOTGIPTVGMAVGILLTTLLVIGIILAVVFI
                                                                                                                                                        VNDNPPRLAKDYTGLFFCHPLSAPGSLIFEAT - - - - DDDQHLFRGPHFTFSLGS - - GSLQ
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                                                             KNWTITRLNGDYAQLSLRIMYLEAGVYDVPIIVTDSGNPPLYNTSIIKVKVCPCDENGDC
                                                                                                                           INDNAPELLPKEAQI-----CEKPNLNVINITAADADIDPNV--GP-FVFELPSVPSAVR
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- AVAAAGLGTGAIIAILICIIILLTMVLL
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P.C.; Hanahan, differential

D ;; express Kell

Jenkins,

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F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-166/Domain: propeptide #status predicted <PRO>
F;167-913/Product: R-cadherin #status predicted <ANT>
F;167-721/Domain: extracellular #status predicted <ANT>
F;169-274/Domain: cadherin repeat homology <CRI>
F;244-249/Region: cadherin binding #status predicted
F;277-389/Domain: cadherin repeat homology <CRI>
F;300-304/Domain: cadherin repeat homology <CRI>
F;307-612/Domain: cadherin repeat homology <CRI>
F;507-612/Domain: cadherin repeat homology <CRI>
F;613-721/Domain: cadherin repeat homology <CRI>
F;613-721/Do
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A;Title: Cell binding specificity of mouse R-cadherin and chromosomal mapping A;Reference number: I55501; MUID:94095672; PMID:8270638
A;Accession: I55501
A;Accession: I55501
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: 1-913 <RES>
A;Residues: 1-913 <RES>
A;Cross-references: GB:D14888; NID:9457658; PIDN:BAA03605.1; PID:9457659
C;Comment: Cadherin; cadherin repeat homology
C;Comment: Cadherin; cadherin repeat homology
C;Keywords: Calcium binding; cell adhesion; duplication; glycoprotein; transme
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                                                                           757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Sinhes 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                         TFSAVDPDREMQQAVRYSKLSDPANWLHINTSNGQITTAAILDRESLYTKNNVYEATFLA
TSVIKVKVCPCDENGDCTTVG---AVAAAGLGTGAIVAILICIVILLIMVLL
                                                                                                                                                                                                   FRGPH-FTFSLGSGSLQNDWEVSKINGTHARLSTRHTDFEERAYVVLIRINDGGRPPLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVTAKDPEGL----DISYSLRGDTRGWLKIDHVTGEIFSVAPLDREA----GSPYRVQVVA
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                                                               IVSLPVTFCSCVEGSCFRPAGHQTGIPTVGMAVGILLTTLLVIGIILAVVFI 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNIVFKAENPEPLVFGVKYNASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVAIGTKVG
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predicted <INT>
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F;162-267/Domain: cadherin repeat homology <CR1>
F;237-242/Region: cadherin binding #status predicted
F;270-382/Domain: cadherin repeat homology <CR2>
F;385-497/Domain: cadherin repeat homology <CR3>
F;500-65/Domain: cadherin repeat homology <CR4>
F;606-712/Domain: cadherin repeat homology <CR4>
F;715-746/Domain: cadherin repeat homology <CR5>
F;715-746/Domain: cadherin repeat homology <CR5>
F;715-746/Domain: cadherin repeat homology <CR5>
F;715-746/Domain: transmembrane #status predicted <TMM>
F;747-906/Domain: homology <CR5>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: this sequence has been revised in reference A38870 R;Walsh, F.S.; Barton, C.H.; Putt, W.; Moore, S.E.; Kelsell, D.; Spurr, N. J. Neurochem. 55, 805-812, 1990 A;Tille: N-cadherin gene maps to human chromosome 18 and 1s not linked to A;Reference number: JQ0751; MUID:90347462; PMID:2384753 A;Accession: JQ0751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Human N-cadherin: nucleotide and A;Reference number: S11487; MUID:91016946; A;Accession: S11487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: cadherin; cadherin repeat homology
C;Keywords: calcium binding; cell adhesion; dupli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-340,'N', 342-698,'R', 700-704,'F', 706-906
A; Cross-references: EMBL: X54315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Reid, R.A.; Hemperly, J.J.
Nucleic Acids Res. 18, 5896, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X54315; NID:g34998; PIDN:CAA38213.1; R;Reid, R.A.; Hemperly, J.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Reid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GDB:128185;
A; Map position: 18q12.1-18q12.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB:CDH2; NCAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
  330
                                                                                                                                                                                                                                                                                                                177 VMYFQINNKTGAISLTREGSQELNPAKNPSYNLVISVKDMGGQSENSFSDTTSVDIIV--
                                                                                                                                                                                                                                                                                                                                                                                                                    117 KDINDNRPTFLOSKYEGSVRONSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLPMINN 176
                                                                                                                                                                                                                                                                                                                                                                      47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cocal Similarity es 210; Conserv
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1te names: N-cadherin; neuronal cadherin
  VKDINDNPPTCPSPVTVFEVQENERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTPKLP
                                                   -----DQPPTGIFIINPISGQLSVTKPLDREQIARFHLRAHAVDINGNQVENPIDIVIN
                                                                                                    YSLVDKEKLPRFPFSIDQ-EGDIYVTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVK 329
                                                                                                                                                          RQFSKHSGHLQRQKRDWVIP-PINLPENSRGPFPQELVRIRSDRDKNLSLRYTVTGPGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 122;
                                                                                                                                                                                                           -TENIWKAPKPVEMVENSTDPHPIKITQVRWN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 699.5; DB 1
Pred. No. 6.7e-36;
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S13799
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N-cacherin precursor, neuronal - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: A29964
C;Accession: A29964
A;Ritta, K.; Nose, A.; Nagafuchi, A.; Takeichi, M.
J. Cell Biol. 106, 873-881, 1988
A;Title: Cloning and expression of cDNA encoding a neural calcium-dependent cell adhesic A;Reference number: A29964
A;McCession: A29964
A;McCession: A29964
A;McCession: A29964; MUID:88153917; PMID:2831236
A;Accession: A29964
A;McCession: A29964; MUID:88153917; PMID:2831236
A;Cross: references: GB:X07277; NID::g63649; PIDN:CAA30258.1; PID::g63650
C;Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought to comment: Cadherins mediate calcium-dependent intercellular adhesion, and cross references: GB:X07277; NID::g63649; PIDN:CAA30258.1; PID::g63650
C;Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought to comment cadherin; cadherin repeat homology
C;Keywords: Calcium binding; cell adhesion; duplication; glycoprotein; transmembrane proficed (PRO)
F;20-164/Domain: signal sequence #status predicted (PRO)
F;20-164/Domain: extracellular #status predicted (PRO)
F;20-20/Domain: cadherin repeat homology (CR1)
F;30-50-50/Domain: cadherin repeat homology (CR2)
F;30-50-50/Domain: cadherin repeat homology (CR3)
F;30-50-50/Domain: cadherin repeat homology (CR3)
F;21-720/Domain: cadherin repeat homology (CR3)
F;21-720/Domain: cadherin repeat homology (CR3)
F;30-50-50/Domain: cadherin repeat homology (CR3)
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F; 721-7
F; 753-9
F; 869-8
F; 278, 3
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                                                                                                                                                                  ;721-752/Domain: transmembrane #status predicted <TMM>
;753-912/Domain: intracellular #status predicted <INT>
;869-884/Region: serine-rich
;278,330,407,578,628,657/Binding site: carbohydrate (Asn) (covalent) #status
126 FLQSKYEGSVRQNSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLPMINNVMYFQIN--
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                                                               1 Similarity
209; Conserv
                                                                                       16.18; 26.98;
                                                      18; Score 696; DB 1; 198; Pred. No. 1.1e-35; 117; Mismatches 328;
                                                                                                               Length
                                                            Indels 124;
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                                                                                             WEVSKINGTHARLSTRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVTFCSC-VEGSCFR
                                  PAGHQTGIPTV---GMAVGILLTTLLVIGIILAVVFIRIKKDKGKDNVESAQASEVKP 829
                                                                                                                                               DINDNAPQVNPKEAT - - - TCETLQ - PNAINITAVDPDIDPNAGP - FAFELPDSPPSIKRN
                                                                                                                                                                                                                       LSDPANWLKIDPVNGQITTTAVLDRESIYVQNNMYNATFLASDNGIPPMSGTGTLQIYLL
                                                                                                                                                                                                                                                                                                                                  ASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVAIGTKVGNVTAKDP----EGLDISYSL
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                                                                       WTIVRISGDHAQLSLRIRFLEAGIYDVPIVITDSGNPHASSTSVLKVKVCQCDINGDC--
                                                                                                                                                                                  DVNDNPPRL-AKDYTGLFFCHPLSAPGSLIFEATDDDQHLFRGPHFTFSLGSG--SLQND
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                                                                                                                                                                                                                                                                                                 POSTATVSITVIDVNESPYFVPNPKLVRQEEGLLAGSMLTTFTARDPDRYMQQTSLRYSK
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N-cadherin precursor, neuronal - mouse
C;Speciaes: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: A32759; A46163
R;Miyatani, S.; Shimamura, K.; Hatta, M.; Nagafuchi, A.; Nose, A.; Matsunaga, M. Science 245, 631-635, 1989
A;Title: Neural cadherin: role in selective cell-cell adhesion.
A;Reference number: A32759; MUID:89346748; PMID:2762814
A;Accession: A32759
A;Molecule type: mRNA
A;Residues: 1-906 <MIY'>
A;Accession: A32759
A;Miyatani, S.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Takeichi, M. Proc. Natl. Acad. Sci. U.S.A. 89, 8443-8447, 1992
A;Title: Genomic structure and chromosomal mapping of the mouse N-cadherin gene
A;Reference number: A46163
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA

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C:Keywords: calcium binding; cell adhesion; duplication; F;1-27/Domain: signal sequence #status predicted <SIG>F;28-159/Domain: propeptide #status predicted <PRO>F;160-906/Product: N-cadherin #status predicted <AMT>F;160-914/Domain: extracellular #status predicted <EXT>F;160-2714/Domain: cadherin repeat homology <CR1>F;162-267/Domain: cadherin binding #status predicted F;162-267/Domain: cadherin binding #status predicted F;270-382/Domain: cadherin repeat homology <CR2>F;385-497/Domain: cadherin repeat homology <CR3>F;300-605/Domain: cadherin repeat homology <CR4>F;500-605/Domain: cadherin repeat hom
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A;Cross-references: GB:945011; NID:9256010; PIDN:AAB23356.1; PID:9256011
A;Cross-references: GB:945011; NID:9256010; PIDN:AAB23356.1; PID:9256011
A;Note: sequence extracted from NCBI backbone (NCBIN:113759, NCBIP:113760)
C;Comment: Cadherins mediate calcium-dependent intercellular adhesion, and C;Superfamily: cadherin; cadherin repeat homology
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                                                                                                                                                                                                                                                                                                  DINDNPPTCPSPVTVFEVQENERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTPKLPMD
LKIKFLEAGIYEVPIIITDSGNPPKSNISILRVKVCQCDSNGDC---
                                                            TRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVTFCSC-VEGSCFRPAGHQTGIPTV---
                                                                                                                                                                                       HPLSA-----PGSLIFEATDDDQHLFRGPH-FTFSLGSGSLQNDWEVSKINGTHARLS
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                                                                                                                           -PQEAETCETPEPNSINIAALDYDIDPNAGPFAFDLPLSPYTIKRNWTINRLNGDFAQLN
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cadherin repeat homology <CR4>
cadherin repeat homology <CR5>
transmembrane #status predicted
intracellular #status predicted
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,572,651,692/Binding site: carbohydrate (Asn) (covalent) #status
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27.6%; Pred. No. 1.40
tive 122; Mismatches
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F;577-685/Domain:
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F;241-353/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S11693; A; Accession: S11693
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F;161,244,296,373
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A; Residues: 1-877 <LIA>
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C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local 203;
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                                                                                                                                                                                                                                                                                           VKDINDNPPTCPSPVTVFEVQENERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTPKLP
                                       DTDPHTNTGYVIIKKPLDFETAAVSNIVFKAENPEPLVFGVKYNASSFAKFTLIVTDVNE
                                                                                                                                                                                                                                                                                                                                            -----DQPPTGIFIINPISGQLSVTKPLDRELIARFHLRAHAVDINGNQVENPIDIVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRSFPLSSEHSKFLIYAQDKE-----TQEKWQVAVKLSLKPALPEDSVKESREIEEIVFP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VMYFQINNKTGAISLTREGSQELNPAKNPSYNLVISVKDMGGQSENSFSDTTSVDIIV--
QTDPNSNDGLVTVVKPIDFETNRMYVLTVAAENQVPLAKGIQHPPQSTATVSVTVIDVNE
                                                                                   DNPPEFTAMTFYGEV----PENRVDVIVANLTVTDKDQPHTPAWNAIYRISGGDPAGRFAI
                                                                                                                             DQIPIF-EKSDYGNLTLAEDTNIGSTILTIQATDADEPFTGSSKILYHIIKGDSEGRLGV
                                                                                                                                                                       SPNMFTINNETGDIITVAAGLDREKVQQYTLIIQATDMEGNPTYGLSNTATAVITVTDVN
                                                                                                                                                                                                              MDGLFLIQTYAGMLQLAKQSLKKQDTPQYNLTIEVSDKD-----FKTLCFVQINVIDIN 443
                                                                                                                                                                                                                                                        VIDMNDNRPEFLHQVWNGTVPEGSKPGTYVMTVTAIDADDPNALNGMLRYRILSQAPSTP
                                                                                                                                                                                                                                                                                                                                                                                   YSLVDKEKLPRFPFSIDQ-EGDIYVTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FPEDVYSAVLSRDVLEGQPLLNVKFSNC-----NGKRKVQYESSEPADFKVDEDGMVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLOSKYEGSVRONSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLP------MINN 176
                                                                                                                                                                                                                                                                                                                                                                                                                             RQVTKHNGYLQRQKRDWVIP-PINLPENSRGPFPQELVRIRSDRDKNLSLRYSVTGPGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLGTGATIATLLCTTTLLTLVLMFVVWMKRRDKERQAKQLLTDP
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n: cadherin binding #status predicted
n: cadherin repeat homology <CR2>
n: cadherin repeat homology <CR3>
n: cadherin repeat homology <CR3>
n: cadherin repeat homology <CR4>
n: cadherin repeat homology <CR5>
n: cadherin repeat homology <CR5>
n: transmembrane #status predicted <INT:
catiential #status predicted <INT:
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,543,593,622,663/Binding site: carbohydrate (Asn) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.9%; Score 688.5; DB 1
26.7%; Pred. No. 3.1e-35;
tive 126; Mismatches 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  species of cadherins PMID:2390969
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APQFSQHVFQAKVSEDVAIGTKVGNVTAKDPEGL---DISYSLRGDTRGWLKIDHVTGEI 619

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cadherin 4 precursor - human
N;Alternate names: R-cadherin
C;Species: Homo sapiens (man)
C;Bete: 13-Sep-1996 *sequence_revision 13-Sep-1996 *text_chan.
C;Cell Regult 2, 261-270, 1991
A;Gete: 13-1916 <SUIZ>
A;Cell Regult 2, 261-270, 1991
A;Cell Regult 2, 1916 *SUIZ>
A;Cell Reg
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F;870-885/Region:
F;283,412,557,632,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Homo sapiens (man)
Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
       290
                                                                                                                                                                                           171
                                                                                                                                                                                                                                     239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         695 AIIAILLCIIILLILVLMEVVWMKRRDKERQAKQLLIDP
                            WVIP-PINVPENSRGPFPQQLVRIRSDKDNDIPIRYSITGVGADQPPMEVFSINSMSGRM
                                                                                                                                                                                                           WKAPKPVEMVENSTDPHPIKITQVRW----NDPGAQYSL--VDKEKLPRFPFSID-QEGDI
  SKPGTYVMTITANDADDSTTANGMVRYRIVTQTPQSPSQNMFTINSETGDIVTVAAGWDR
                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain: transmembrane #status
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                                                                                          YVTRPMDREEHASYHLRAHAVDMNGNKVENPIDLYIYVIDMNDNHPEFINQVYNCSVDEG
                                                                                                                                  YVTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEVQEN
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                                                                                                                                                                                                                                                                                                   Similarity
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,661,702/Binding
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                                                                                                                                                                                                                                                                                                     15.8%;
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                                                                                                                                                                                                                                                                                                   Score 684.5;
Pred. No. 6e-
                                                                                                                                                                                                                                                                                                                                                                   site: carbohydrate (Asn) (covalent)
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C;Species: Brachydanio rerio (zebra fish)
C;Date: 13-Sep1996 #sequence_revision 13-Sep-1996 #text_change
C;Accession: I50116
R;Bitzur, S; Kam, Z; Geiger, B.
Dev. Dyn. 201, 121-136, 1994
A;Title: Structure and distribution of N-cadherin in developing
A;Reference number: I50116; MUID:95178741; PMID:7873785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-783 <BIT>
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I50116
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Best Local Similarity
Matches 187; Conserv
467
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                                                                                                                                                                                                                                                    YVTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEVQEN
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STILTIQATDADEPFTGSSKILYHIIKGDSEGRLGVDTDPHTNTGYVIIKKPLDFETAAV 526
                                          EKVPQYTLIIQATDMEGNPTYGLSNTATAVIRLLDVNDNAPEFTRETFHGEVPENRVNVI
                                                                                     QDTPQYNLTIEVSDKD-----FKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTNIG
                                                                                                                                    AKPGTFVMTVTSQDKDDPNTANGMLRYKILSQTPESPSSNMFTINNKTGKIITVAAGLDR
                                                                                                                                                            SVTKPLDREHIPNFHLRAHAVDINGNQMENPIDIIINVIDMNDNRPEFTHQIWNGTVDEG
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R; Kawamura, K.; Watanabe, K.; Suzuki, T.; Yamakawa, T.; Kamiyama, J. Biol. Chem. 269, 26295-26302, 1994
A;TItle: CDNA cloning and expression of a novel human desmocollin. A;Reference number: A53363; MUID:95014464; PMID:7929347
A;Accession: B55363
A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
B55363
C;Specles: Homo sapiens (man)
C;Specles: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-May-1997
C;Accession: B55363
R;Kawamura, K; Watanabe, K; Suzuki, T.; Yamakawa, T.; Kamiyama, T.; Nakag:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: cadherin; cadherin repeat homology C;Keywords: alternative splicing; transmembrane p F;138-243,Domain: cadherin repeat homology <CRl>F;246-355/Domain: cadherin repeat homology <CR2>
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A; Residues: 1-826 < KAW>
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  ETAAVSNIVFKAENPEPLVFGV-KYNASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVA
                                        ENAFNVEILRIPIEDKDLINTANWRVNFTILKGNENGHFKISTDKETNEGVLSVVKPLNY
                                                                    DTNIGSTILTIQATDADEPFTGSSKILYHIIKGDSEGRLGVDTDPHTNTGYVIIKKPLDF
                                                                                                                                                                                              VLESSRPGTTVGVVCATDRDEPDTMHTRLKYSILQQTPRSP--GLFSVHPSTGVITTVSH
                                                                                                                                                                                                                      VQENERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTPKLPMDGLFLIQTYAGMLQLAKQ
                                                                                                                                                                                                                                                                          NLFCTRPVDREEYDVFDLIAYASTADGYSADL--PLPLPIRVEDENDNHPVFTEAIYNFE
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                                                                                                                    YLDREVVDKYSLIMKVQDMDGQFFGLIGTSTCI--ITVTDSNDNAPTFRQNAYE--AFVE
                                                                                                                                                      SLKKQDTPQYNLTIEVSDKDFK-----TLCFVQINVIDINDQIPIFEKSDYGNLTLAE
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R:Kawamura, K.; Watanabe, K.; Suzuki, T.; Yamakawa, T.; Kamiyama, J. Biol. Chem. 269, 26295-26302, 1994

A:Title: cDNA cloning and expression of a novel human desmocollin. A:Reference number: A55363; MUID:95014464; PMID:7929347

A:A:Recession: A55363
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                                                                                                                                                                                                                                                                                                                                                                           DIYVTQPLDREEKDAY--VEYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EENRQVNLEIGVNNEAPFARDIPRVTALNRALVTVHVRDLDEGPECTPAAQYVRIKENLA
                                                                                                                                                                                                                                                                          VLESSRPGTTVGVVCATDRDEPDTMHTRLKYSILQQTPRSP--GLESVHPSTGVITTVSH
                                                                                                                                                                                                                                                                                          VQENERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTPKLPMDGLFLIQTYAGMLQLAKQ 408
                                                                                                                                                                                                                                                                                                                                                    NLFCTRPVDREEYDVFDLIAYASTADGYSADL--PLPLPIRVEDENDNHPVFTEAIYNFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVQVVATEVGGSSLSSVSEFHLILMDVNDNPPRLAKDYTGLFFCHPLSAPGSLIFEATDD
                                                                                                                    ENAFNVEILRIPIEDKDLINTANWRVNFTILKGNENGHFKISTDKETNEGVLSVVKPLNY
                                                                                                                                                                                                                      SLKKQDTPQYNLTIEVSDKDFK-----TLCFVQINVIDINDQIPIFEKSDYGNLTLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKKDKGK 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAGQAATKLLRVNLCECTHPTQCRATSRSTGVILGKWAILAILLGIALLESVLLTLVCGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEPVHGAP-FYFSLPNTSPEISRLWSLTKVNDTAARLSYQKNAGFQE--YTIPITVKD--
                                                                              ETAAVSNIVFKAENPEPLVFGV-KYNASSFAKETLIVTDVNEAPQFSQHVFQAKVSEDVA
                                                                                                                                                        DTNIGSTILTIQATDADEPFTGSSKILYHIIKGDSEGRLGVDTDPHTNTGYVIIKKPLDF
                                                                                                                                                                                              YLDREVVDKYSLIMKVQDMDGQFFGLIGTSTCI--ITVTDSNDNAPTFRQNAYE--AFVE
                                          EENRQVNLEIGVNNEAPFARDIPRVTALNRALVTVHVRDLDEGPECTPAAQYVRIKENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.5%;
30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     compared with conceptual translation
  ·GLDISYSLRGDTRGWLKIDHVTGEIFSVAPLDREAGSP----Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 671.5; DB 2
Pred. No. 3.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 07-May-1999
C;Accession: Ad0390; S16464
R;Parker, A.E.; Wheeler, G.N.; Arnemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            k;Parker, A.E.; Wheeler, G.N.; Arnemann, J.; Pidsley, S.C.; Ataliotis, P.; Thomas, C.L.; J. Biol. Chem. 266, 10438-10445, 191
A;Title: Desmosomal glycoproteins II and III. Cadherin-like junctional molecules generat A;Reference number: A40390; MUID:91244819; PMID:2037591
A;Accession: A40390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-847 <PAR>
A; Cross-references: GB: X56807
A; Note: It is uncertain whether Met-1 is the initiator or whether translation is initiat
A; Note: It is uncertain whether Met-1 is the initiator or whether translation is initiat
A; Note: Note: It is uncertain whether Met-1 is the initiator or whether translation is initiat
A; Note: It is uncertain whether Met-1 is the initiator or whether translation is initiat
A; Out: It is uncertain whether Met-1 is the initiator or whether translation is initiator.
A; Buxton, R.S.; Cowin, P.; Franke, W.W.; Garrod, D.R.; Green, K.J.; King, I.A.; Koch, P.
J. Cell Biol. 121, 481-483, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;29-135/Domain: propeptide #status predicted <PRO>
F;136-847/Product: desmocollin 3b #status predicted <EXT>
F;136-695/Domain: extracellular #status predicted <EXT>
F;138-243/Domain: cadherin repeat homology <CR1>
F;246-355/Domain: cadherin repeat homology <CR2>
F;358-471/Domain: cadherin repeat homology <CR3>
E;358-471/Domain: cadherin repeat homology <CR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 18q12.1-18q12.1
C; Superfamily: cadherin; cadherin repeat homology C; Keywords: alternative splicing; calcium binding; F; 1-20/Domain: signal sequence #status predicted <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: GDB:DSC3; DSC2; DSC1; DS
A;Cross-references: GDB:126552; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Contents: annotation; nomenclature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Nomenclature of the desmosomal cadherins. A; Reference number: A43032; MUID:93252984; PMID:8486729
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                                                                                                                                                                     137 W-APIPCSMLENSLGPFPLFLQQVQ-SDTAQNYTIYYSIRGPGVDQE--PRNLFYVERDT 192
                                                                                                                                                                                                  239 WKAPKPVEMVENSTDPHPIKITQVRWNDPGAQYSL------VDKEKLPRFPFSIDQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         715 FGATKGK 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                810 IKKDKGK 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 694 DQHLFRGPHFTFSLGSGS--LQNDWEVSKINGTHARLS-TRHTDFEERAYVVLIRINDGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               634 RVQVVATEVGGSSLSSVSEFHLILMDVNDNPPRLAKDYTGLFFCHPLSAPGSLIFEATDD
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                                                                                                                                                                                                                                                                                                       Local
QENERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTPKLPMDGLFLIQTYAGMLQLAKQS 409
                                                         GNLYCTRPVDREQYESFEIIAFATTPDGYTPELPLPLIIKIEDENDNYPIFTEETYTFTI
                                                                                               GDIYVTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEV
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                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                           ,629/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane *status predicted <TMM>
intracellular *status predicted <INT>
                                                                                                                                                                                                                                                                                                          15.4%;
                                                                                                                                                                                                                                                                                                                                                                                           carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OMIM: 600271
                                                                                                                                                                                                                                                                          Score 667.5; DB 1;
Pred. No. 6.2e-34;
4; Mismatches 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <SIG>
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                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                21;
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A;Title: Desmosomal glycoproteins II and III. Cadherin-like A;Reference number: A40390; MUID:91244819; PMID:2037591
A;Accession: B40390
                                                 F;29-135/Domain: propeptide #status predicted <PRO>F;136-901/Product: desmocollin 3a #status predicted <MAT>F;136-695/Domain: extracellular #status predicted <EXT>F;136-695/Domain: cadherin repeat homology <CR1>F;138-243/Domain: cadherin repeat homology <CR2>F;246-355/Domain: cadherin repeat homology <CR2>F;358-471/Domain: cadherin repeat homology <CR3>F;358-471/Domain: cadherin repeat homology <CR4>
                                                                                                                                                                                                                                                                                                    A;Gene: GDB:DSC3; DSC2; DSC1; DS
A;Cross-references: GDB:126552; OMIM:600271
A;Map position: 18q12.1-18q12.1
C;Superfamily: cadherin; cadherin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A43032; MUID:93252984; A; Contents: annotation; nomenclature C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:X56807
A;Note: it is uncertain whether Met-1 is the initiator or whether translation is R;Buxton, R.S.; Cowin, P.; Franke, W.W.; Garrod, D.R.; Green, K.J.; King, I.A.; K., Cell Biol. 121, 481-483, 1993
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                                                                                                                                                                                                                                                C; Keywords: alternative splicing; calcium binding; cel F;1-28/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Nomenclature of the desmosomal cadherins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-901 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 07-May-1999 C;Accession: B40390; S16465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IJHUDA
desmocollin 3a precursor - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNGIYNITVLASDQGGRTCTGT--LGIILQDVNDNSPFIPK--KTVIICKPTMSSAEIV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDRELIDKYQLKIKVQDMDGQYFGLQTTSTCIINIDDVNDHLPTFTRTSY--VTSVEENT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKKQDTPQYNLTIEVSDKD-----FKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTN 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FENCRYGTTYGQVCATDKDEPDTMHTRLKYSIIGQVP--PSPTLFSMHPTTGVITTTSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDGGRPPLEGIVSLPVTFCSCV-EGSCFRPAGHQTGIPTVGMAVGILLTTLLVIGIILAV 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EATDDDQHLFRGPHFTFSLGSGS--LQNDWEVSKINGTHARLSTRHTDFEERAYVVLIRI 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KENAEVGTTSNGYKAYDPETRSSSGIRYKKLTDPTGWVTIDENTGSIKVFRSLDREAETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEDVAIGTKVGNVTAKDPE---GLDISYSLRGDTRGWLKIDHVTGEIFSVAPLDREA---
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F;166,392,546,629/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;864/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.4%; Score 667.5; DB 1; Best Local Similarity 30.9%; Pred. No. 6.9e-34; Matches 186; Conservative 104; Mismatches 253;
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711 LF 712
                                806 VF 807
                                                                                                                                                                                             541 KNGIYNITVLASDQGGRTCTGT--LGIILQDVNDNSPFIPK--KTVIICKPTMSSAEIV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 FENCRYGTTYGQYCATDKDEPDTMHTRLKYSIIGQVP--PSPTLFSMHPTTGVITTTSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 WKAPKPVEMVENSTDPHPIKITQVRWNDPGAQYSL-----VDKEKLPRFPFSIDQE- 289
                                                                                                                          - AVDPDEPI-HGPPEDESLESSTSEVQRWWRLKAINDTAARLSYQN-DPPEGSYVVPITV
                                                                                                                                                                                                                                                            SEDVAIGTKVGNVTAKDPE---GLDISYSLRGDTRGWLKIDHVTGEIFSVAPLDREA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKKQDTPQYNLTIEVSDKD-----FKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTN 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QENERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTPKLPMDGLFLIQTYAGMLQLAKQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDIYVTQPLDREEKDAYVEYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEV
                                                               RD--RIGMSSYTSLDYTLCDCITENDCTHRVDPRIGGGGVQLGKWAILAILLGIALLFCI
                                                                                            NDGGRPPLEGIVSLPVTFCSCV-EGSCFRPAGHQTGIPTVGMAVGILLTTLLVIGIILAV 805
                                                                                                                                                   EATDDDQHLFRGPHFTFSLGSGS--LQNDWEVSKINGTHARLSTRHTDFEERAYVVLIRI
                                                                                                                                                                                                                                                                                                                               QQMILQIGVVNEAPFSREASPR----
                                                                                                                                                                                                                                                                                                                                                           -----TAAVSNIVEKAE-NPEPLVEGVKYNASSEAKETLIVTDVNEAPQESQHVEQAKV 575
                                                                                                                                                                                                                                                                                                                                                                                                                              IGSTILTIQATDADEPFTGSSKILYHIIKGDSEGRLGVDTDPHTNTGYVIIKKPLDFE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDRELIDKYQLKIKVQDMDGQYFGLQTTSTCIINIDDVNDHLPTFTRTSY--VTSVEENT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNLYCTRPVDREQYESFEIIAFATTPDGYTPELPLPLIKIEDENDNYPIFTEETYTFTI
                                                                                                                                                                                                                   -GSPYRVQVVATEVGGSSLSSVSEFHLILMDVNDNPPRLAKDYTGLFFCHPLSAPGSLIF
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                                                                                                                                                                                                                                                                                                                               ----SAMSTATVTVNVEDQDEGPECNPPIQTVRM
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Search completed: January 15, 2003, 08:18:23 Job time: 66.7352 secs

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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
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            Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1 MILQAHLHSLCLLMLYLATG......DKGKDNVESAQASEVKPLRS 832
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Gapop 10.0 , Gapext 0.5
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CADH_ROTE
CADH_RAT
CADG_HUMAN
CADG_HUMAN
CADG_HUMAN
CAD2_HOUSE
CAD2_HUMAN
CAD2_HOUSE
CAD2_HUMAN
CAD2_RAT
CAD2_HUMAN
CAD2_RAT
CAD4_HUMAN
DSC2_HUMAN
DSC3_HUMAN
DSC3_HUMAN
DSC3_HUMAN
DSC3_HOVIN
CADD_HUMAN
DSC3_BOVIN
CADD_HUMAN
DSC3_HOUSE
CAD1_CHICK
CAD1_RAT
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Q2863338
P199023
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5 homo sapien
8 mus musculu
8 gallus gall
8 mus musculu
1 homo sapien
8 gallus gall
6 mus musculu
4 bos taurus
3 rattus norv
7 homo sapien
7 kenopus lae
6 bos taurus
6 homo sapien
7 kenopus lae
7 kenopus lae
8 bos taurus
8 homo sapien
9 taurus
1 apien
1 pallus gall
1 gallus gall
1 rattus norv
4 homo sapien
7 homo sapien
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mus musculu
       EMBL; U07969; AAA19021.1; EMBL; X83228; CAA58231.1; HSSP; P15116; INCJ. Genew; HGNC:1756; CDH17. MIM; 603017; -.
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SMART; SM00112; CA; 5
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Pfam; PF00028; cadherin;
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              FTGSSKILYHIIKGDSEGRLGVDTDPHTNTGYVIIKKPLDFETAAVSNIVFKAENPEPLV
                                                          TIEVSDKDFKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTNIGSTILTIQATDADEP
                                                                          TIEVSDXDFKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTNIGSTILTIQATDADEP
                                                                                                                    EEKDAYVFYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEVQENERLGNSIG
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CADHERIN-17.
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Pred. No. 7.1e-256;
Mismatches 0;
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16-OCT-2001 (Rel. 40, 1
15-JUN-2002 (Rel. 41, 1
15-JUN-2002 (Rel. 41, 1
Cadherin-17 precursor (
cadherin) (P130).
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                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., SEQUENCE OF 26
490-509, TISSUE SPECIFICITY, AND D
STRAIN-BALB/C; TISSUE-Fetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                STRAIN-Swiss Webster; TISSUE-Angres B., Kim L., Tauber R.;
                                                                                                                                                                                                                                                                                     MEDLINE-20469471;
                                                                                                                                                                                                                                                                                                                                             Submitted
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(AUG-1999)
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                                                                                                                                                                                                                                                                                                                                                       expression
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EMBL/GenBank/DDBJ databases.
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                                                      adhesion; Glycoprotein;
TGSSKILYHIIKGDSEGRLGVDTDPHTNTGYVIIKKPLDFETAAVSNIVFKAENPEPLVF
                          IEVSDKDFKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTNIGSTILTIQATDADEPF
                                                                                         EKDAYVEYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEVQENERLGNSIGT
                                                                                                                    PKPVEMVENSTDPHPIKITQVRWNDPGAQYSLVDKEKLPRFPFSIDQEGDIYVTQPLDRE
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                                                                                  EKNSHVFFATAKDENGKPLAYPLETYVKVIDINDNPPTCLSPVTVFEVQENEPLGNSIGI
                                                                                                             PEPVETRENSTDPHPIKITOVOWNDPGAQYSLVNKEKLSPFPFSIDQEGNIYVTQALDRE
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658; Conservative
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Pred. No. 8
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SMART; S
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                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berndorff D., Gessner R., Kreft B., Schnoy N., Lajous-Petter A.-M. Loch N., Reutter W., Hortsch M., Tauber R.; "Liver-intestine cadherin: molecular cloning and characterization a novel Ca(2+) dependent cell adhesion molecule expressed in liver
                              PROSITE; PS00232; CADHERIN_1; 3.
PROSITE; PS50268; CADHERIN_2; 6.
Cell adhesion; Glycoprotein; Transmembrane;
                                                                                                             InterPro; IPR002126; Cad
Pfam; PF00028; cadherin;
                                                                                                                                            EMBL; X78997; CAA55631.1; HSSP; P15116; INCI.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Cell Biol. 125:1353-1369(1994).

FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTE THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO . SORTING OF HETEROGENEOUS CELL TYPES. LI-CADHERIN MAY HAVE A FINT THE MORPHOLOGICAL ORGANIZATION OF LIVER AND INTESTINE.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: LIVER AND INTESTINE.
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SM00112; CA; 6.
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EXTRACELLULAR
POTENTIAL.
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Pred. No. 1.3e-200;
D; Mismatches 102;
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HSSP; P09803; 1SUH.
InterPro; IPR002126; Cadh
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MEDLINE-95340560; PubMed-
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TISSUE SPECIFICITY: KIDNEY-SPECIFIC. LIMITED T
MEMBRANES OF RENAL TUBULAR EPITHELIAL CELLS.
SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
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Chordata; Craniata; Vertebrata;
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Last sequence update)
Last annotation update)
(Kidney-specific cadherin) (Ksp-cadherin).
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               CADHERIN 16.
EXTRACELLULAR
POTENTIALS
CYTOPLASMIC (POCADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 6.
ECTODOMAIN 6.
ECTODOMAIN G.
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                                                                                                                                                                                                                                                                                                                                  Transmembrane;
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D2DF10E6C47A43B9
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                                                                                                                                                                                                                                                                                                                                  Calcium-binding; Repeat;
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   CRC64;
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(POTENTIAL).
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16-OCT-2001
15-JUN-2002
Cadherin-16
                                                                                              CADG_HUMAN
075309;
              Homo sapiens (Human)
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Local Similarity
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                                                                                                                                                                                                                                                                                  -YSFALGPNPTVQRDWRLQPLNDSHAFLTLALHWVEPREHIVPVVVSQDAR-----VWQL
                                                                                                                                                                                                                                                                                                                                                     DAPRLSTSAALVIHFLRAPPAPALPLAPMPSRHLCTPRQDHGVLIPAPSEDPDMATGHGP
                                                                                                                                                                                                                                                                                                                                                                                                           FLLTIQPAEPWNGALRFSLVNDSEGWFCIQKVSGEVHTARPLQGARPGDSYTVLVEAQDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTLVATLTATDADLEP---AFRLMDFTIEAGDGEGTFGLDWEPDSGHVQLYLLKNLSYEA
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 Metazoa;
                                       (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation updat
precursor (Kidney-specific cadh
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                                                                                                             STANDARD;
Chordata;
                                                                                                                                                                                                             832
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 Craniata;
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                                        update)
c cadherin)
 Vertebrata;
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 Euteleostomi;
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Best Local S
Matches 237
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SEQUENCE
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CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF016272; AAC34255.1; HSSP; P09803; 1SUH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isoforms of Ksp-cadherin.";
Genomics 51:445-451(1998).
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Thomson R.B., Ward
Aronson P.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00232; CADHERIN_1; PROSITE; PS50268; CADHERIN_2;
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                                      237
                                                                              177
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                                                                                                                                                                                                                                                                     62 LTGE----TDNIFVIERE-GLLYYNRALDRETRSTHNLQVAALDANGIIVEGPVPITIEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETEROGENEOUS CELL TYPES.
SUBCELLULAR LOCATION: Type I membrane protein (Probable).
TISSUE SPECIFICITY: KIDNEY-SPECIFIC.
SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
                                      NIWKAPKPVEMVENSTDPHPIKITQVRWNDPGAQYSLVDKEKLPRFPFSIDQEGDIYVTQ
                                                                                                   VMYFQINNKTGAISLTREGSQELNPAKNPSYNLVISVKDMGGQSENSFSDTTSVDIIVTE
                                                                                                                                                                                    KDINDNRPTFLQSKYEGSVRQNSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLPMINN
STWVSLEPIHLAENLKVLYPHHMAQVHWSGGDVHYHL---ESHPPGPFEVNAEGNLYVTR
                                                                                                                                                                                                                                           PDMFQLEPRLGALALSPKGSTSLDHALERTYQLLVQVKDMGDQA-SGHQATATVEVSIIE
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                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                              Conservative
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d D.C., Quaggin
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                                                                                                                                                                                                                                                                                                                              163;
                                                                                                                                                                                                                                                                                                                                                                                                            WW.
                                                                                                                                                                                                                                                                                                                                                                                                      Score 922.5; DB 1;
Pred. No. 9.2e-49;
63; Mismatches 353;
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"Ksp-cadherin gene promoter. I. Se epithelial-cell-specific activity. Submitted (JAN-1999) to the EMBL/G-I- FUNCTION: CADHERINS ARE CALCIU
                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                   "Ksp-cadherin gene prom
                                                          Whyte D.A.,
                                                                    STRAIN-129/Sv;
                                                                                                    "cDNA cloning and chromosomal isoforms of Ksp-cadherin."; Genomics 51:445-451(1998).
                                                                                                                                     Aronson
                                                                                                                                                Thomson
                                                                                                                                                         STRAIN-BALB/c;
MEDLINE-98389630;
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                                             Thomson R.B., Nix S.L., ., Igarashi P.;
                                                                                                                                               Ward D.
                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                         PubMed-9721215;
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                                                                                                                                                                                                               Chordata;
Rodentia;
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Last annotation updat
(Kidney-specific cadh
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     CALCIUM
              EMBL/GenBank/DDBJ
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Sciurognathi; Muridae
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c cadherin) (Ksp-cadherin).
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00232; PROSITE; PS50268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00028; cadherin; SMART; SM00112; CA; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF016271; AAC34254.1; EMBL; AF118228; AAF28836.1;
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SUBCELLULAR LOCATION: Type I membrane protein (HISSUE SPECIFICITY: KIDNEY-SPECIFIC.
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                                                                                                                                                                                                                                                                        LTGETD----NIFVIERE-GLLYYNRALDRETRSTHNLQVAALDANGIIVEGPVPITIEV
           LKKQDTPQYNLTIEV--
                                                                                                                                       NIWKAPKPVEMYENSTDPHPIKITQVRWNDPGAQYSLVDKEKLPRFPFSIDQEGDIYVTQ
                                                                                                                                                                                                                             KDINDNRPTFLQSKYEGSVRQNSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLPMINN
                                 TETARLSAEDLDAPGSPNSHIVYQLLSPEPEEGAENKAFELDPTSGSVTLGTAPLHAGQS
                                                     NSIGTLTAHDRDEENTANSFLNYRIVEQTPKLPMDG-LFLIQTYAGMLQL----
                                                                            ELDREAQAEYQLQVRAQNSHGEDYAEPLELQVVVMDENDNAPVCSPHDPTVNIPELSPPG
                                                                                                 PLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEVQENERLG
                                                                                                                         NSWAPLEPVHLAENLKVVYPHSIAQVHWSGGDVHYQL---ESQPPGPFDVDTEGMLHVTM
                                                                                                                                                                     PDMFQLDPHLGALALSPSGSTSLDHALEETYQLLVQVKDMGDQPSGHQAIAT-VEISIVE
                                                                                                                                                                                          VMYFQINNKTGAISLTREGSQELNPAKNPSYNLVISVKDMGGQSENSFSDTTSVDIIVTE
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519
667
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89859
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CADHERIN_2;
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rin; 6.
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-SDKDFKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTNIGS
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Pred. No. 5.1e
41; Mismatches
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CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
CADHERIN 6.
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N-LINKED (GLCNAC...
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CYTOPLASMIC
CADHERIN 1.
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1. No. 5.1e-46;
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RESULT 7

CAD4_CHICK
ID 24503
AC P24503
AC CD44.
OS GALlus
OC Archos
OC Archos
OC Archos
OC Archos
OC Archos
AC MCBI_T
RP SEQUEN
RC TISSUE
RX MEDIUN
RA INUZUK
RT "R-Cad
RT express
RL Neuron
CC -1- FU
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AN INUZUKA H., MİYALANİ S., TAKƏİCHİ M.;
AN INUZUKA H., MİYALANİ S., TAKƏİCHİ M.;
AN INUZUKA H., MİYALANİ S., TAKƏİCHİ M.;
AN INUZUKA H., MİYALANİ S., TAKƏİCHİ M.;
AN INUZUKA H., MİYALANİ S., TAKƏİCHİ M.;
AN INUZUKA H., MİYALANİ S., TAKƏİCHİ M.;
AN INUZUKA H., MİYALANİ S., TAKƏİCHİ AN INDESION MOLECULE
AN INUZUKA H., TAKƏİCHİ MƏRİMININ MAY THENSION PROTEINS.
C. THEY PREFERBITIALLY INVERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETERCENEOUS CELL TYPES. MAY PLAY AN IMPORTANT ROLE
C. SORTING OF HETERCENEOUS CELL TYPES. MAY PLAY AN IMPORTANT ROLE
C. IN RETINAL DEVELOPMENT.
C. IN RETINAL DEVELOPMENT.
C. SUBCELLULAR LOCATION: Type I membrane protein.
C. IN SUBCELLULAR LOCATION: TYPE I MEMBRYONIC BRAIN AND NEURONAL RETINA.
C. INTISSUE SPECIFICITY: EMBRYONIC BRAIN AND NEURONAL RETINA.
C. INTISSUE SPECIFICITY: EMBRYONIC BRAIN AND NEURONAL RETINA.
DIFFERBATIATION HAS TAKEN PLACE AND PERSISTS AT LEAST UP TO THE
C. NEWLY HATCHED STAGE.
C. INTILARITY: CONTAINS 5 CADHERIN DOMAINS.
                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for conmodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cadherin-4 precursor (Retinal-cadherin) (R-cadherin) (R-CAD)
                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
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HSSP; P15116; 1NCI.
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InterPro; IPR000233; Cadherin_C_term
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FQSTAGVTISVTDVNEAPYFPTNHKLIRLEEGVPTGTVLTTFSAVDPDRFMQQAVRYSKL
                                 AIYRIISGDPSGHFTIRTDPVTNEGMVTVVKAVDYEMNRAFMLTVMVSNQAPLASGIQMS
                                                  ILYHIIKGDSEGRLGVDTDPHTNTGYVIIKKPLDFETAAVSNIVFKAENPEPLVFGVKYN
                                                                                --FKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTNIGSTILTIQATDADEPFTGSSK
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                                                                                                                                          VDMNGNKVENPIDLYIYVIDMNDNRPEFINQVYNGSVDEGSKPGTYVMTVTANDADDSTT
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                                                                     YGLSNTATAIITVTDVNDNPPEFTTSTYSG--EVPENRVEVVVANLTVMDRDQPHSPNWN
                                                                                                       ANGMVRYRIVTQTPQSPSQNMFTINSETGDIVTVAAGLDREKVQQYMVIVQATDMEGNLN
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26.9%;
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MEDLINE-94095672; PubMed-8270638;
Matsunam1 H., Miyatani S., Inoue T.
Jenkins N.A., Takeichi M.;
"Cell binding specificity of mouse of the gene.";
J. Cell Sci. 106:401-409(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAD4_MOUSE STANDARI
P39038;
01-FEB-1995 (Rel. 31, C
01-FEB-1995 (Rel. 31, I
16-OCT-2001 (Rel. 40, I
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TISSUE-PANCREATIC ISlets;
MEDLINE-94067164; PubMed-824;
Hutton J.C., Christofori G.,
Hanahan D., Kelly R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDH4.
                                  HSSP;
                                                          EMBL;
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                 BL; X69966; CAA49589.1; -
BL; D14888; BAA03605.1; -
R; A47543; A47543.
BP; P15116; INCI.
                                                                                                                                                                                                Cell Sci. 106:401-409(1993).

Cell Sci. 106:401-409(1993).

THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADMERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. MAY PLAY AN IMPORTANT ROLE IN RETINAL DEVELOPMENT.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: DISTRIBUTED WIDELY IN MOUSE TISSUES WITH HICLEVELS PRESENT IN BRAIN, SKELETAL MUSCLE, AND THYMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus
                                                                                                                                           veen the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                         SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
                                                                                                                             SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
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an email to license@isb-sib.ch).
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A Wallis J.A., FOX M., Walsh F.S.;
T "Structure of the human N-cadherin gene: YAC analysis and f chromosomal mapping to 18q11.2.";
Genomics 22:172-179(1994).
C -1- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOP MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBU SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE NEURONAL RECOGNITION MECHANISM.
C -1- SUBCELLULAR LOCATION: Type I membrane protein.
C -1- SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
                                                                                      EMBL; X57548; CAA40773.1; ...
EMBL; X54315; CAA38213.1; ...
EMBL; X42303; AAB22854.1; ...
EMBL; M34064; AAA03236.1; ...
EMBL; 277420; CAA81799.1; ...
PJR; A38B70; IJHUCUN.
HSSP; P15116; INCJ.
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P19072; 014923;
01-NOV-1990 (Rel. 16, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neural-cadherin (Rel. 40, Cast annotation update)
Neural-cadherin (Rel. 40, Cast annotation (Cadherin-2)
Neural-cadherin (Rel. 40, Cast annotation (Cadherin-2)
CDH2 OR CDHN OR NCAD.
Homo saplens (Human).
                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"N-cadherin gene maps
E-cadherin gene.";
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MEDLINE-91016946; PubMed-2216790;
Medline-91016946; PubMed-2216790;
Reid R.A., Hemperly J.J.;
"Human N-cadherin: nucleotide and dedu
Nucleic Acids Res. 18:5896-5896(1990).
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Avaion O., Patel-King
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InterPro; IPR002126; Cadherin.
InterPro; IPR000233; Cadherin_C_term.
Pfam; PF00028; Cadherin; 5.
Pfam; PF01049; Cadherin_C_term; 1.
PRINTS; PR00205; CADHERIN.
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between
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MEDILIND-88153917; PubMed-2831236;

MEDILIND-88153917, PubMed-2831236;

Hatta K., Nose A., Nagafuchi A., Takeichi M.;

"Cloning and expression of cDNA encoding a neural calcium-dependent cell adhesion molecule: its identity in the cadherin gene family.";

Cell Biol. 106:873-881(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Cornish white rock Cockerel;
MEDLINE-97354288; PubMed-9210582;
Li B., Paradies N.E., Brackenbury R.W.;
"Isolation and characterization of the
                                                                                                                                                                                                 EMBL; X07277; CAA30258.1;
EMBL; U15563; AAB62980.1;
PIR; A29964; IJCHCN.
HSSP; P15116; INCJ.
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Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified
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                                                                                                                                                                                                                                                                                                                                                                                                   send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e 191:7-13(1997).
FUNCTION: CACHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTIFER PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOCHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO SCRIING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEURONAL RECOGNITION MECHANISM.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration veen the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGLGTGAIIAILLCIIILLILVLMFVVWMKRRDKERQAKQLLIDP
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                                                                                                                                                                                                                                                                                                                                                                                           s requires a license agreement (
an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-profit institutions as long and this statement is not removed
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PROSITE; PS00232; CADHERIN_1;
PROSITE; PS50268; CADHERIN_2;
Cell adhesion; Glycoprotein; ;
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 DINDNAPQVNPKEAT - - -
                   DVNDNPPRL-AKDYTGLFFCHPLSAPGSLIFEATDDDQHLFRGPHFTFSLGSG-
                                                                                              ASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVAIGTKVGNVTAKDP----
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                                                   RGDTRGWLKIDHVTGEIFSVAPLDREA---
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P15116; Q64
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P15116; Q64260;
O1-APR-1990 (Rel. 14, Created)
O1-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                               Neuron 20:1153-1163(1998)
                                                                                                                                                                                                                                     MEDLINE-95191680; PubMed-7885471;
Shapiro L., Fannon A.M., Kwong P.
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Miyatani S., Shinamura K., Hatta M., Nagafuchi
Matsunaga M., Hatta K., Takeichi M.;
"Neural cadherin: role in selective cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDH2
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                                                                                                         cadherin
                                                                                                                                MEDLINE-98318235;
Tamura K., Shan W.
                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS)
                                                                                                                                                                                   "Structural basis of cell-cell adhesion Nature 374:327-337(1995).
                                                                                                                                                                                                              Hendrickson
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                                                                                                                                                                                                                                                                                                                                                       STRAIN~C57BL/6; TISSUE=Test1s;
MEDLINE=97033837; PubMed=8879495;
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"Genomic structure and chrom
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Miyatani S., Copeland N.G., Gilbert
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            MANNER IN CONNECTING CELLS; CAL
SORTING OF HETEROGENEOUS CELL I
NEURONAL RECOGNITION MECHANISM.
SUBCELLULAR LOCATION: Type I me
                                     FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS. THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMODHILIC MANUER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED 1
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Legrand J.-F., Als-Nielsen
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.S., Hendrickson W.A.,
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Pfam; PF01049; Cadherin_C_term;
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InterPro; IPR002126; Cadherin.
InterPro; IPR000233; Cadherin_C_term.
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European Bioinformatics Institute
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Institute. There are no re
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
מחוירים (Arcadherin precursor (N-cadherin) (Cad
                                                This
                                                                                                                                                                                  EMBO
                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-90360979; PubMed-2390969;
Liaw C.W., Cannon C., Power M.D., Kiboneka
"Identification and cloning of two species
    the
                                  between
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Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
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                                                                     O J. 9:2701-2708(1990).

FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTE FUNCTION: CADHERINS ARE CALCIUM THEMSELVES IN A HOMOPHILIC THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLV NEURONAL RECOGNITION MECHANISM.

SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR LOCATION: Type I membrane protein.
SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no was
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InterPro; IPR000233; Cadherin_C_term.
Pfam; PF00028; cadherin; 5.
Pfam; PF01049; Cadherin_C_term; 1.
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                    DTDPHTNTGYVIIKKPLDFETAAVSNIVFKAENPEPLVFGVKYNASSFAKFTLIVTDVNE
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                                         DNPPEFTAMTFYGEV---PENRVDVIVANLTVTDKDQPHTPAWNAIYRISGGDPAGRFAI
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CADHERIN 2.
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                                                                                                                   EMBL; AF097593; AAC83818.1;
EMBL; AB017695; BAA84919.1;
HSSP; P15116; INCJ.
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16-OCT-2001 (Rel. 40, Last annotation update)
Neural-cadherin precursor (N-cadherin) (Cadherin-2).
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                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 5 CADHERIN DOMAINS
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"Diversity of the cadherin family: evidence for eight new cadherins in nervous tissue.";

Cell Regul. 2:261-270(1991).

-1- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

THEY PREFERENTIALL INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. MAY PLAY AN IMPORTANT ROLE IN RETINAL DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tanihara H., Sano K., Heimark R.L., St John T., Suzuki S.; "Cloning of five human cadherins clarifies characteristic fe cadherin extracellular domain and provides further evidence structurally different types of cadherin."; Cell Adhes. Commun. 2:15-26(1994).
                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-Fetal brain;
TISSUB-Fetal brain;
MEDLINE-91283540; PubMed-2059658;
Cano K. Tanihara H.;
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Mammalia; Eutheria;
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P55283;
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                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Type I I
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Pfam; PF01049; Cadherin_C_
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                                                                             GPYVFELPFVPAAVRKNWTITRLNGDYAQLSLRILYLEAGMYDVPIIVTDSGNPPLSNTS
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A Jenkins N.A., Gilbert D.J., Copeland N.G.,
Missed desmocollin (Dsc3) and desmoglein (Dsg1) genes are closely
at linked in the proximal region of chromosome 18.";
Ilnked in the proximal region of chromosome 18.";
Genomics 21:510-516(1994).
C. IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS
C. IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS
C. MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERWAL CELL
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C. SUBCELULAR LOCATION: Type I membrane protein
C. INTERNATIVE PRODUCTS: 2 ISOFORMS; AND SB ARE
C. PRODUCED BY ALTERNATIVE SPLICING.
C. INTERNATIVE SPLICING.
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STRAIN-C57BL/6; TISSUE-Embryo;
MEDLINE-9527276; PubMed-7711832;
LOTIMET J.E., Hall L.S., Clarke J.P., Collins J.E., Flem Garrod D.R.;
"Cloning, sequence analysis and expression pattern of modesmocollin 2 (DSC2), a cadherin-like adhesion molecule. Mol. Membr. Biol. 11:229-236(1994).
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Desmocollin 2A/2B precursor (Epithelial type
InterPro; IPR002126; Cadherin.
InterPro; IPR00023; Cadherin_C_term.
Pfam; PF00028; cadherin; 5.
Pfam; PF00028; Cadherin_C_term; 1.
Pfam; PF000205; Cadherin_C_term; 1.
PRINTS; PR00205; CADHERIN.
SMART; SM00112; CA; 5.
PROSITE; PS00232; CADHERIN_1; 3.
PROSITE; PS00232; CADHERIN_2; 5.
Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal; Alternative splicing; Cytoskeleton; Calcium-binding.
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EMBL;
HSSP;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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O8r490 rattus norv
Q9wul0 rattus norv
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Q9qxa3 mus musculu
Q8r508 rattus norv
Q9v5n8 drosophila
Q9vw71 drosophila
Q9vw71 drosophila
                                                                                   Q9haz9 homo sapien
Q8tbx3 homo sapien
Q8vdk4 mus musculu
Q77704 canis famil
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Q90x63 brachydanio
Q8uvq7 brachydanio
P79883 xenopus. ma
Q90275 brachydanio
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ALIGNMENTS

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                                                                                                                                               KA Erickson R.H., Gum J.R. Jr., Lindstrom M.M., McKean D., Kim Y.S.;
RT "Regional expression and dietary regulation of rat small intestinal
RT peptide and amino acid transporter mRNAS.";
RL Biochem. Biophys. Res. Commun. 216:249-257(1995).
CC -1 - SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
DR EMBL; 146874; AAC42077.1; -.
DR HSSP; P15116; 1NCJ.
DR InterPro; IPR002126; Cadherin.
DR Pfam; PF00028; cadherin; 6.
DR SMART; SM00112; CA; 6.
DR PROSITE; PS00232; CADHERIN_1; 1.
R PROSITE; PS00232; CADHERIN_1; 1.
R PROSITE; PS0268; CADHERIN_2; 6.
CALcium-binding; Cell adhesion; Glycoprotein.
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SEQUENCE
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STRAIN-WISTAR; TISSUE-SMALL INTESTINE;
MEDLINE-96067558; PubMed-7488096;
Erickson R.H., Gum J.R. Jr., Lindstrom M.M.,
                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Proton-driven peptide transporter (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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77.3%; Pred. No. 4.30
tive 55; Mismatches
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                                                    Horsfield J., Ramachandran A., Reuter K., LaVallie E.
Collins-Racie L., Crosier K., Crosier P. Sr.;
"Zebrafish cadherin-17 is required for pronephric duc
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databas
-i- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
EMBL; AF428098; AAL29444.1; -
RINGERPRO; IPRO02126; Cadherin.
Pfam; PF00028; cadherin; 6.
Pfam; PF00028; cadherin; 6.
PROSITE; PS00232; CADHERIN 1; UNKNOWN_2.
RPOSITE; PS00232; CADHERIN 2; 6.
Calcium-binding; Cell adhesion; Glycoprotein.
Calcium-binding; Cell adhesion; Glycoprotein.
                           Query Match
Best Local
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CDH17.

Brachydanio rerio (Zebrafish) (
Bukaryota: Metazoa; Chordata; C
Actinopterygii; Neopterygii; Te
Cyprinidae; Danio.
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O90X63;
O1-DEC-2001 (Tremburel. 1
O1-DEC-2001 (Tremburel. 1
O1-MAR-2002 (Tremburel. 2
                                                                                                                                                               SEQUENCE FROM N.A.
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Cyprinidae; Danio.
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Ostariophysi; Vertebrata;

Euteleostomi; Cypriniformes;

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Query Match
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InterPro; IPR000233; Cadherin.C_term.
InterPro; IPR000215; Serpin.
Pfam; PF00028; Cadherin; 5.
Pfam; PF01049; Cadherin.C_term; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00232; CADHERIN_1; UNKNOW PROSITE; PS50268; CADHERIN_2; 3. PROSITE; PS00284; SERPIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lele Z., Folchert A., Concha M., Kauch G., Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Bally-Cuif L., Hammerschmidt Wilson S.W., Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wilson Wi
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74
                                                                                                                                                                                                                                                                                               LFFCHPLSA-----PGSLIFEATDDDQHLFRGPHFTFSLGS--GSLQNDWEVSKINGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIPTDPVTNEGLVTVVKPVDFEMNRSFMLTVVADNEVPLASGIHRTRQSTATVSIRVIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVDTDPHTNTGYVIIKKPLDEETAAVSNIVFKAENPEPLVFGVKYNASSFAKFTLIVTDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DINDQIPIFEKSDYGNLTLAEDTNIGSTILTIQATDADEPFTGSSKILYHIIKGDSEGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVKVKDINDNPPTCPSPVTVFEVQENERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QYSLV--DKEKLPRFPFSIDQ-EGDIYYTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEI
TVGMAVGILLTTLLVIGIILAVVFIRIKKDKGKDNVESAQASEVKP
                                                                                                                                                                                                                                                                                                                                                                                                          RISTIAVLDRESPYVKNNLYNATFMASDNGVPRASGTGTLQIYLLDINDNAPRV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIFSVAPLDREA----GSPYRVQVVATEVGGSSLSSVSEFHLILMDVNDNPPRLAKDYTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEAPQFSQHVFQAKVSEDVAIGTKVGNVTAKDPEGL---DISYSLRGDTRGWLKIDHVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYSVTGPGADQNPTGLFIIDPISGLLSVTKPLDREHIPNFHLRAHAVDINGNQMENPIDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVDIIV----IKITQVRWNDPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----FRI-DADGTVMAAR--TLQLTDRKGQS--LEIKAKDENSQEQWMVHINFTQPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MINNVMYFQINNKTGAISLTREGSQELNPAKNPSYNLVISVKDMGGQSE----NSFSDTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QPGFTENEYNVMTADVITEGQVLLKVDFVDCGRGSGLRFESGDPAD-----
                                                                             HAQLSLKISYLESGIYELPISITDSGNLPMSNTTYLRIKVCQCDHHGDCV----DMERIM
                                                                                                                                                          HARLSTRHTDFEERAYVVLIRINDGGRPPLEGIVSLPVTFCSC-VEGSCFRPAGHQTGIP
                                                                                                                                                                                                                                           ----FPQEAEVCERPEPNAINITAVDGDLNPNAGP-YAFELPNRPSDIRRNWTLTRISGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NESPNFDPNPKQIKLEEGLPQWSMLTTFTAHDPDRYMQQTISYSKLYDPANWLEIDPNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVNDNAPEFTRETFHGEVPENRVNVIVTNLTV--TDKDEPGTPAWNAVYRIISGDPTGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESPSSNMFTINNKTGKIITVAAGLDREKVPQYTLIIQATDMEGNPTYGLSNTATAVIRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLPMDGLFLIQTYAGMLQLAKQSLKKQDTPQYNLTIEVSDKD-----FKTLCFVQINVI 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TINVIDMNDNRPEFTHQIWNGTVDEGAKPGTFVMTVTSQDKDDPNTANGMLRYKILSQTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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27.8%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Concha M., Rauch G.-J., Geisler R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115;
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Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNKNOWN_3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103;
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Best Local Similarity
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PROSITE; PS50268; CADHERIN_2; 3.
Calcium-binding; Cell adhesion; Glycoprotein.
Calcium-binding; Cell adhesion; FEA7A95CBAF1B640 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00205; CADHI
SMART; SM00112; CA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; S82457; AAB37685.2; HSSP; P15116; INCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and expression studies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae.
NCBI_TaxID=8353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; (Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-JUN-2002 (TrEMBLrel. 21, Maternally expressed neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00028; cadherin; 5.
Pfam; PF01049; Cadherin_C_term;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002126; Cadherin.
InterPro; IPR000233; Cadherin_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (XmN-cadherin),
embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-TAIL BUD;
MEDLINE-96257964; PubMed-8652409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MN-CADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: TYPE I MEN-!- SIMILARITY: CONTAINS 3 CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tashiro K., Tooi O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                   177
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h. Dev. 54:161-171(1996).

h. Dev. 54:161-171(1996).

FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANUAL THUS: CONTRIBUTE TO THE MANUAL TO THE THE THE THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES (BY SIMILARITY).

SORTING OF HETEROGENEOUS CELL TYPES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GETDNIFVIEREGLLYYNRALDRETRSTHNLQVAALDANGIIV----EGPVPITIEVKDI
-EGDIYVTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASVSSAC-----TPGFSADG-YTALVSP---NIMEGQKLLKVKFNGCSSGAQGIWYE-T
                                                                                                               VTENIWKAPKPVEMVENSTDPHPIKITQVRWN---DPGAQYSL--VDKEKLPRFPPSIDQ
                                                                                                                                                                                                                                               FQINNKTGAISLTREGSQE-----LNPAKNPSYNLVISVKDMGGQSENSFSDTTSVDII
                                                                                                                                                                                                                                                                                                                                                         NDNRPTFLQSKYEGSVRQNSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLPMINNVMY
                                                                                                                                                                                                                                                                                                                                                                                                           NNPD--FKVGADGAVY-----TAREVQIPAKQAKFIVAAWDHETP------
                                                                                   WVIP-
                                                                                                                                                                                             -TG--
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                                                                                                                                                                                                                                                                                                    -EKWEAAIQ---
                                                                                   PVNVPENSRGPFPQQLVLIRSDKDRDDTIRYSITGVGADQPPMAIFNIDP
                                                                                                                                                                                             SQSQESEQEQSQSGTLLPWRQHHKGLRRQKRD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; ; Anura; Me
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Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation updat
cadherin XmN-cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 699; DB 13;
Pred. No. 2.3e-37;
0; Mismatches 334;
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Q90275;
                                                                                                                         Bitzur S., Kam Z., Geiger B.;

"Structure and distribution of N-cadherin in developing zebrafisl morphogenetic effects of ectopic over-expression.";

Dev. Dyn. 201:121-136(1994).

-i- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTI THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED.
                                                                                                                                                                                                                                                                                                                               Actinopterygii; Neopterygii; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Zebra danio)
Eukaryota; Metazoa; Chordata; Craniata; Ver
                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Neural-cacherin precursor (N-cacherin).
CDH2 OR CDH2 OR ZNCAD.
                                                                                                                                                                                                                                                                     TISSUE-EMBRYO
                                                                                                                                                                                                                                                   MEDLINE-95178741; PubMed-7873785;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
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REURONAL RECOGNITION MEDIANISM.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSION IN THE EMBRYO IS INITIALLY FOUN
ALL DEEP CELLS BUT LATER BECOMES RESTRICTED TO VARIOUS EPITHEI
AND NEURONAL TISSUES. FOUND IN DISCRETE AREAS OF CELL-CELL
ADHESION WHEN EPIBOLY IS NEARLY COMPLETED. EXPRESSED IN ADULT
BRAIN, EYES AND TRUNK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTKVGNVTAKDPE---GLDISYSLRGDTRGWLKIDHVTGEIFSVAPLDREAGSP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YRVQVVATEVGGSSLSSVSEFHLILMDVNDNPPR-LAKDYTGLFFCHPLSAPGSLIFEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMSKVFPLIVMVTNQAPLASGIQMSLQSTAAVTVSVNDVNEAPYFPNRNEPIRKLEGESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETAAVSNIVFKAENPEPLVFGVKYNASSFAKFTLIVTDVNEAPQFSQHVFQAKVSEDVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENHVDVVVANLTVVDRDQPYTSNWNAVFKIISGDPDGHFTIKTDPVTNEGIVTVSKPVDY
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                                                                                                                                                                                                                                                                                  TISSUE
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                                                                                                                                                                        ADHESION PROTEINS
                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                             Cypriniformes;
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                                                              EPITHELIAL
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PROSITE; PS50268; CADHERIN_2; 5.
Cell adhesion; Glycoprotein; Phosphorylation;
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Pfam; PF01049; Cadherin_
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InterPro; IPR000233; Cadherin_C_term
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SIMILARITY: BELONGS TO
L; X67648; CAA47890.1;
P; P15116; 1NCI.
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                                               NVTA-KDPEGL---DISYSLRGDTRGWLKIDHVTGEIFSVAPLDREA----
                                                                                       VINLTV--TDKDEPGTPAWNAVYRIISGDPTGRESIPTDPVINEGLVTVVKPVDFEMNRS
                                                                                                                           STILTIQATDADEPETGSSKILYHIIKGDSEGRLGVDTDPHTNTGYVIIKKPLDFETAAV
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                   ATEVGGSSLSSVSEFHLILMDVNDNPPRLAKDYTGLFFCHPLSA-----PGSLIFEAT
                                      TFTAHDDPDRYMQQTISYSKLYDPANLLEIDPNNGRISTIAVLDRESPYVKNNLYNATFM
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01-MAR-2001 (TrEMBLrel. 16
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
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SEQUENCE FROM N.A.

MEDLINE=20484176; PubMed=11027496;
Whittock N.V., Hunt D.M., Rickman L., Malhi S., Vogaziano
Whittock N.V., Hunt D.M., Rickman L., McGrath J.A.;

Whittock N.V., Eady R.A., Buxton R.S., McGrath J.A.;

"Genomic organization and amplification of the human desm
cadherin genes DSC1 and DSC3, encoding desmocollin types
Biochem. Biophys. Res. Commun. 276:454-460(2000).

-1- SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.

EMBL, AF293359, AAG23427.1; -.

HSSP; P15116; INCJ.
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PROSITE; PS50268; CADHERIN_2; 5.
Calcium-binding; Cell adhesion;
SEQUENCE 839 AA; 93497 MW; F
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID-9606;
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Pred. No. 1.3e-35;
6; Mismatches 263;
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Matches 192
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Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ
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01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Cadherin 13, H-cadherin (heart).
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Mammalia; Eutheria;
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PATGAWRAAYTIINGNPGQSFEIHTNPQTNEGMLSVVKPLDYEISAFHTLLIKVENEDPL
                                            PFTGSSKILYHIIKGDSEGRLGVDTDPHTNTGYVIIKKPLDFETAAVSNIVFKAENPEPL
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01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00232; CADHERIN_1;
PROSITE; PS50268; CADHERIN_2;
SEQUENCE 714 AA; 78116 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0205; CADHERIN. SMART; SM00112; CA; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
EMBL; BC021638; AAH21628.1; -.
InterPro; IPR002126; Cadherin.
Pfam: PF00028; Cadherin; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8VDK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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                                                                      NIRQQTPDKPSPNMFYIDPEKGDIVTVVSPALLDRETLENPKYELIIEAQDMAGLDVGLT
                                                                                                                                                                                              LSYPLEIHVKVKDINDNPPTCPSPVTVFEVQENERLGNSIGTLTAHDRDEENTANSFLNY
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                                                                                                              RIVEQTPKLPMDGLFLIQTYAG-MLQLAKQSLKKQDT---PQYNLTIEVSDK-----DFK
                                                                                                                                                               LEGPVPLEVIVIDQNDNRPIFREGPYIGHVMEGSPTGTTVMRMTAFDADDPATDNALLRY
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39; Conservative
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Rodentia;
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29.3%;
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Pred. No. 1.9e
.09; Mismatches
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CA5CA791C46A2FFB
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01-NOV-1998 (
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HSSP; P09803; 1SUH.
InterPro; IPR002126; Cadherin.
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Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                    PROSITE; PS00232; CADHERIN_1; 2.
PROSITE; PS50268; CADHERIN_2; 4.
Calcium-binding; Cell adhesion; Glycoprotein.
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                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                   Buxton R.
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                                                                                                  W-APIPCSMQENSLGPFPLFLQQIQ-SDTAQNYTIFYSIRGPGVDRE--PKNLFYVERDT
                        QENERLGNSIGTLTAHDRDEENTANSFLNYRIVEQTPKLPMDGLFLIQTYAGMLQLAKQS
                                                                       GDIYVTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTCPSPVTVFEV
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SENCRVGSTVGQVCATDKDEPDTMHTRLKYSIIEQLPAYPT--LFSMHPATGVITTSSSQ
                                                 GNLFCTRPVDREEYESFELIAFATTPDGYTPELPLPLVIRIEDENDNYPIFTEKTYVFTI
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8 (TrEMBLrel. 08, Las:
2 (TrEMBLrel. 21, Las:
n type 2 (Fragment).
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91081 MW;
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08, Last sequence update)
21, Last annotation updat
                                                                                                                                                Score 651.5; I
Pred. No. 2.5e
10; Mismatches
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Canis.
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Best Local Similarity
Matches 188; Conserv
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O1-JUN-2002 (TrEMBLrel.:

O1-JUN-2002 (TrEMBLrel.:

O1-JUN-2002 (TrEMBLrel.:

T-cadherin.
                                                                                                                                                                                                                                                                                                                                     Niermann T., Schmutz S.;
"Cloning of rat T-cadherin.";
"Cloning (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AF494095; AAM14607.1; ".
SEQUENCE 714 AA; 78085 MW; 7E56142B8162F864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8R490
                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-HEART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKKQDTPQYNLTIEVSDKD-----FKTLCFVQINVIDINDQIPIFEKSDYGNLTLAEDTN
NIRQQTPDKPSPNMFYIDPEKGDIVTVVSPALLDRETLENPKYELIIEAQDMAGLDVGLT
                                                                    LSYPLEIHVKVKDINDNPPTCPSPVTVFEVQENERLGNSIGTLTAHDRDEENTANSFLNY
                                                                                                                           ND--PGAQYSLVDK--EKLPRFPFSIDQE-GDIYVTQPLDREEKDAYVFYAVAKDEYGKP
                                                                                                                                                                  GGKDIQGSLQDIFKFARTSPVPRQKRSIVVS
                                                                                                                                                                                 SVKDMGGQSEN--SFSDTTSV----DIIVTENIWKAPKPVEMVENSTDPHPIKITQVRW
                                                                                                                                                                                                                          NKKLHYEV-----
                                                                                                                                                                                                                                                   NGQLYYQIVIQLPMINNVMYFQINNKTGAI---SLTREGSQELNPAKNPSYN-----LVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- RHGRSLITPLKVLLCDCVTENDCTLRTDARTGGGDVRLGKWAILAILLGIALLFCILF
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                       RIVEQTPKLPMDGLFLIQTYAG-MLQLAKQSLKKQDT---PQYNLTIEVSDK-----DFK
                                                      LEGPVPLEVIVIDQNDNRPIFREGPYIGHVMEGSPTGTTVMRMTAFDADDPATDNALLRY
                                                                                                              SDRPEGSKFRLTGKGVDQDPKGTFRINENTGSVSVTRTLDRETIATYQLFVETTDASGRT
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                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                          -SSPYFKVNSDGTLVAVRNITAVGRTLFVHARTPHAEDMAELVIV
                                                                                                                                                                                                                                                                               15.0%; Score 650; DE 29.1%; Pred. No. 2.6e tive 110; Mismatches
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Last sequence update)
Last annotation update)
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Sciurognathi; Muridae;
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                                                                                                                                                               -----PILIPENQRQPFPRDVGKVVD
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2.6e-34;
les 287;
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; Murinae; Rat
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Pfam; PF000054; laminin_G;
PRINTS; PR00205; CADHERIN.
SMART; SM00112: Ca. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9WU10;
01-NOV-1999
01-NOV-1999
01-JUN-2002
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM NO....
STRAIN-SPRACUE-DAWLEY:
STRAIN-SPRACUE-DAWLEY:
MEDLINE-99173791: PubMed-10072790;
MEDLINE-99173791: PubMed-10072790;
MEDLINE-99173791: PubMed-10072790;
MEDLINE-99173791: PubMed-10072790;
MEDLINE-99173791: PubMed-10072790;
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MEDLINE-99173791: PubMed-10072790;
MEDLINE-99173791: PubMed-10072790;
                                                                                               SMART;
SMART;
SMART;
                              PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00232; CADHERIN_1; 16.
PROSITE; PS50268; CADHERIN_2; 33.
PROSITE; PS00022; EGF_1; UNKNOWN_4.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
                                                                                                                                                                                                                                                    -!- SIMILARITY: CONTAINS 33
EMBL; AF100960; AAD20459.1;
HSSP; P01132; 1EGF.
                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 Hydroxylation; SEQUENCE 458
          Calcium-binding; Cell adhesion; Hydroxylation; Repeat.
                                                                                                                                                                                                                                                                                               suppressor
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                                                                                                                                                                                                                                                                                     Mech.
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                                                                                                                                                                                                                                                                                     essor gene.";
Dev. 80:207-212(1999).
                                                                                                SM00001;
SM00282;
                                                                                                                    SM00112;
SM00179;
                                                                                                                                                                                                         IPR002126;
IPR000561;
IPR000742;
                                                                                                                                                                                 IPR000742; EGF_2.
IPR001881; EGF_Ca.
IPR001791; Laminin_G.
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                                                                                                                                                              cadherin; 33
EGF; 5.
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; EGF_CA; 1.
; EGF_like; 2.
; LamG; 1.
                                                                                                                                                     laminin_G; 1.
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                                                                                                                                                                                                                   ; Asx_hydroxyl.; Cadherin.; EGF-like.
 505987 MW;
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                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
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                      EGF-like
 8CD0561B1DC58677 CRC64;
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the Drosophila fat
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                      domain; Glycoprotein;
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on update)
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Murinae; Rat
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Best Local Similarity
Matches 228; Conserv
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                                                                                                                                EVNQ---
                                                                                                                                                         EVSKINGTHARLSTRHTDFE--ERAYVVLIRINDGGRPPLEGIVSLPVTFCSCVEGSCFR
                                                                                                                                                                                                                {\tt LMDVNDNPPRLAKDYTGLFFCHPLSAPGSLIFEATDDDQHLFRGPHFTFSLGSGSLQNDW}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKYEGSVRONSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLPMINNVMYFQINNKTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DROSGRIKLEKSLDHETTKWYQFSILARCTLDDYEVVAS--IDVSIQVKDANDNSPVLES
                                                                         3545
                                                                                                    776
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  PRELIMINARY;
                                                                                                                               -HGVLLTAATVKRKVKDHYLLHVKVADNGKPQLSSLTHIDI---RVIEESIHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PSPVTVFEVQENERLGNSIGTLTAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.5%; Score 628; DB 11;
25.3%; Pred. No. 1.3e-31;
Live 135; Mismatches 329
  PRT;
  4587
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Best Local S
Matches 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COX B.T.M., Hadjantonakis A.K., Collins J., Magee A.I.;

"Cloning and expression throughout mouse development of mf
nomologue of the Drosophila tumour suppressor gene fat.";

Lev. Dyn. 217:233-240(2000).

-!- SIMILARITY: CONTAINS 33 CADHERIN DOMAINS.

REMBL; AJZ50768; CAB65271.1; -.

R HSSP; P08709; 1BF9.

R InterPro; IPR001216; Cadherin.

R InterPro; IPR00181; EGF-Cike.

R InterPro; IPR00181; EGF-Cike.

R InterPro; IPR00179; Laminin_G.

R InterPro; IPR00179; Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9QXA3;

O1-MAY-2000 (TrEMBLrel. 13, Created)

O1-MAY-2000 (TrEMBLrel. 13, Last sequence up

O1-JUN-2002 (TrEMBLrel. 21, Last annotation

Mouse fat 1 cadherin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00232; CADHERIN_1; 16.
PROSITE; PS50268; CADHERIN_2; 33.
PROSITE; PS00022; EGF_1; UNKNOWN_2.
Calcium-binding; Cell adhesion; Glycoprotein.
NON_TER 4587 4587
SEQUENCE 4587 AA; 506036 MW; 4D3F23BB0512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
SMART;
SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
                                 3036
                                                                                                                                                                2925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00008; EGF; 4.
Pfam; PF00054; laminin_G; 1.
PRINTS; PR00205; CADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000561; EGF-lik
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001791; Laminin
Pfam; PF00028; cadherin; 33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20203461; PubMed=10741417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
 341
                                                                                                                                                                                                                                                             189
                                                                                                                                                                                                                                                                                                                                                                                            73
                                                                                                                                                                                                                                                                                                                                                                                                                                               26 KFSGPLKPMTFSIYE----GQEPSQIIFQ-----FKANPPAVTFELTGETDNIFVI 72
                                                                                                                                                                                                                                                                                                                                                           ERE-GLLYINRALDRETRSTHNLQVAA---LDANGIIVEGPVPITIEVKDINDNRPTFLQ 128
                                                                                                                              DIYVTQPLDREEKDAYVFYAVAKDEYGKPLSYPLEIHVKVKDINDNPPTC-----
                                                                                                                                                                                                WKA-----
                                                                                                                                                                                                                                                                                             SPYEAFIVENLPGGSRVIQIRASDLDSGA--NGQVMYSL-DQSQDADIIESFAINMETGW 2870
                               EDALPGKLVMQVSATDADIRSNAEITYTLFGSGAEKFKLNPDTGELRTLALLDREEQAVY 3095
                                                                                                                                                              YKGTVSEDDPPGGVIAILSTTDADTEEINR-----QVSYFITGGDALGQFAVENVQSDW
                                                                                                                                                                                                                                                             ISLTREGSQELNPAKNPSYNLVISVKDMGGQSENSFSDTTSVDIIVTE-----NI
                                                                                                                                                                                                                                                                                                                             SKYEGSVRQNSRPGKPFLYVNATDLDDPATPNGQLYYQIVIQLPMINNVMYFQINNKTGA 188
                                                                                               RVYVKKPLDREQKDSYLLTVTATD---GTFSSKARVEVKVLDANDNSPVCEKTSYSDTIP 3035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SM00112; CA; 31.
; SM00179; EGF_CA; 1.
; SM00001; EGF_like; 1
; SM000282; LamG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                              ELDHEERASYQIKVVASDHGEKVQ--LSSTAIVGVTVTDVNDSPPRFTAEI
                                                                                                                                                                                              -PKPVEMVENSTDPHPIKITQVRWNDPGAQYSLVDKEKLPRFPF-SIDQEG
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LamG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.4%;
25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2.5e
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 624; DB 11;
Pred. No. 2.5e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4D3F23BB05127CB4 CRC64;
-PSPVTVFEVQENERLGNSIGTLTAH 365
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                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 225
                                                      2775
                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 290:1260-1266(2002). EMBL; AB076401; BAB86869.1; -. SEQUENCE 4555 AA; 502077 MW; B47CBC10638EA73B C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8R508;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitsui K., Nakajima D., Ohara O., Nakayama M.; "Mammalian fat3: a large protein that contains EGF-like motifs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
MEDLINE-21670969; PubMed-11811999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3372
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  146
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LYVNATDLDDPATPNGQLYYQIVIQLPMINNVMYFQINNKTGAISLTREGSQELNPAKNP
                                                SPAFHFKVAATIPLDKVDIVF--TVDVDVKVLDLNDNKPVFETSSYETIIMEGMPVGTKL 2832
                                                                                                                                                          PNQSVRFSTVNGERPE---
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                                                                                                    RSTHNLQVAA----LDANGIIVEGPVPITIEVKDINDNRPTFLQSKYEGSVRQNSRPGKPF
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                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                            14.1%; Score 611; DB 11; Length 4555;
25.4%; Pred. No. 1.7e-30;
Live 144; Mismatches 320; Indels 196
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                                                                                                                                                             Q9V5N8;

Q9V5N8;

Ol-MAY-2000 (TrEMBLrel. 13, Created)

TOL-MAR-2001 (TrEMBLrel. 16, Last sequence update)

TOL-MAR-2001 (TrEMBLrel. 21, Last annotation update)

TOL-JUN-2002 (TrEMBLrel. 21, Last annotation update)

PROTOCADHERIN-like wing polarity protein STAN precursor

protein) (FLAMINGO protein).

STAN OR CG11895 OR FMI.

STAN OR CG11895 OR FMI.

S Drosophila melanogaster (Fruit fly).

EUKARYOLA; Metazoa; Arthropoda; Tracheata; Hexapoda; Insterioridea; Metazoa; Endopterygota; Diptera; Brachycera;

Ephydroidea; Drosophilidae; Drosophila.
MEDLINE=20025940; PubMed=10556066; Chae J.W., Kim M.-J., Goo J.H., Co Adler P.N., Park W.J.;
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                                                                                         TISSUE=EMBRYO
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                                                                                                           SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The Drosophila tissue polarity gene starry night encodes a member the protocadherin family.";
Development 126:5421-5429(1999).
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PROSITE; PS00232; CADHERIN_1; 5.

PROSITE; PS00268; CADHERIN_2; 8.

PROSITE; PS00022; EGF_1; 4.

PROSITE; PS01186; EGF_2; 3.

PROSITE; PS01227; G_PROTEIN_RECEP_F2_3; 1.

PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.

PROSITE; PS50261; G_PROTEIN_TYPE_EGF; 1.
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pF02793; HRM; 1.
pF00053; laminin
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)5; CADHERIN.
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 hormn_receptor.
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                                     VGVNAQITYSLNEESINGLG-SPDPFSINPQTGAIVTNAPLDRETTSGYLLTVTAKD-
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RA Ballew R.M., Basun A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beleson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botchier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,
RA Buttis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Codson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferriaz C., Ferriara S., Fleischmann W.,
Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mchulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Watssenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Watssenbach J.,
RA Wang X.-Y., Wassarman D.A., Weinstock G.M., Watssenbach J.,
RA Wang X.-Y., Shong F.M., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.M., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.M., Zhong W., Zhou X., Smith H.O.,
RA Shue B.C., Scheeler J.C., Zhoo Q., Zheng L.,
RA Zheng X.H., Zhong S., Zhou X., Smith H.O.,
RA Shue B.C., Scheeler J.C., Zhoo Q., Zheng L.
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Q9VW71;
01-MAY-2000
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Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative fat-like CG7749.
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(TIEMBLIEL 13, Last sequence update)
(TIEMBLIEL 21, Last annotation update)
t-11ke cadherin precursor (CG7749 protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachycera;
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InterPro; IFR000152; Asx_hydroxyl.
InterPro; IFR000126; Cadherin.
InterPro; IFR000181; EGF-11ke.
InterPro; IFR0001881; EGF-Ca.
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